

Delaval, Jan

91408

From: Ewoldt, Gerald
Sent: Tuesday, April 15, 2003 10:09 AM
To: Delaval, Jan
Subject: seq search for 09/521,527

Jan,
Please search SEQ ID NO:1, closed and including interference.

Thanks,
Gerry

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PS Claim 1: Page 15; 21pp; English.

CC The present invention describes a method for isolating CD8+ cells (1)
CC from peripheral mononuclear blood cells (PBMC) using an antibody which
CC specifically binds to the sequence AAEGLDTRFSG (1) or a portion of (1)
CC on CD8 molecules present on the surface of CD8+ cells but does not
CC activate the CD8+ cells once bound. Also described are: (1) a hybridoma
CC cell line (II) which produces a monoclonal antibody that specifically
CC binds to CD8 molecules present on the surface of CD8+ cells but does not
CC activate the CD8+ cells; (2) a monoclonal antibody (III) produced by
CC (III) (3) a polypeptide comprising (1), useful for generating (III);
CC (III) and an agent which causes the dissociation of CD8+ cell-antibody
CC complex. (1) is useful for isolating human CD8+ cells from a sample of
CC isolated peripheral mononuclear blood cells. The isolated CD8+ cells have
CC importance as vehicles for combating viral infections and tumours.

SO Sequence 12 AA:

Query Match 100.0%; Score 60; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGLDTRFSG 12
Db 1 AAEGLDTRFSG 12

RESULT 2
AAB24102 standard; peptide; 11 AA.

AC AAB24102;
XX
XX 23-JAN-2001 (first entry)
XX
XX Human CD8 antigenic peptide CD8-3.
XX
XX Human: CD8; antibody; antigenic; viral infection; tumour;
XX CD8+ cell; peripheral mononuclear blood cell.
XX
XX Homo sapiens.
XX
XX MO200055305-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000MO-US05898.
XX
XX 12-MAR-1999; 99US-0124253.
XX
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX
XX Leturcq D;
XX
XX WPI: 2000-618917/59.
XX
XX Isolating CD8+ cells from peripheral mononuclear blood cells for use as
XX vehicles for combating viral infections and tumors, comprises using a
XX CD8 specific antibody that does not activate the cells
XX
XX Disclosure: Page 8; 21pp; English.

CC The present invention describes a method for isolating CD8+ cells (1)
CC from peripheral mononuclear blood cells (PBMC) using an antibody which
CC specifically binds to the sequence AAEGLDTRFSG (1) or a portion of (1)
CC on CD8 molecules present on the surface of CD8+ cells but does not
CC activate the CD8+ cells once bound. Also described are: (1) a hybridoma
CC cell line (II) which produces a monoclonal antibody that specifically
CC binds to CD8 molecules present on the surface of CD8+ cells but does not
CC activate the CD8+ cells; (2) a monoclonal antibody (III) produced by
CC (III) (3) a polypeptide comprising (1), useful for generating (III);
CC (III) and an agent which causes the dissociation of CD8+ cell-antibody
CC complex. (1) is useful for isolating human CD8+ cells from a sample of
CC isolated peripheral mononuclear blood cells. The isolated CD8+ cells have
CC importance as vehicles for combating viral infections and tumours.

CC (III) and an agent which causes the dissociation of CD8+ cell-antibody
CC complex. (1) is useful for isolating human CD8+ cells from a sample of
CC isolated peripheral mononuclear blood cells. The isolated CD8+ cells have
CC importance as vehicles for combating viral infections and tumors. The
CC present sequence represents a human CD8 antigenic peptide designated
CC CD8-3, which is given in the exemplification of the present invention.

SO Sequence 11 AA:

Query Match 90.0%; Score 54; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGLDTRFSG 11
Db 1 AAEGLDTRFSG 11

RESULT 3
AAR98502 standard; peptide; 8 AA.

AC AAR98502;
XX
XX 04-MAR-1997 (first entry)
XX
XX CD8 alpha chain residues 60-67.
XX
XX CD8 antagonist; inhibitor; T-cell activation; human; CD8 alpha chain;
XX thymic differentiation; transplantation; bone marrow; liver; heart; lung;
XX kidney; cornea; skin graft; graft versus host disease; therapy.
XX
XX Homo sapiens.
XX
XX MO9622106-A1.
XX
XX 25-JUL-1996.
XX
XX 17-JAN-1996; 96MO-US00310.
XX
XX 17-JAN-1995; 95US-0372952.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Choksi S, Huang Z, Jameson BA, Kornigold R;
XX
XX WPI: 1996-354307/35.
XX
XX CD8 antagonist peptide(s) - used for inhibiting T cell activation,
XX partic. for treating transplant rejection or graft versus host
XX disease
XX
XX Claim 2; Page 28; 44pp; English.

CC AAR98501-R98505 represent components of a CD8 antagonist of the
CC invention. These sequences are fragments of the human CD8 alpha chain
CC molecule (see AAR98514). This sequence corresponds to residues 60-67 of
CC the human CD8 sequence. CD8 plays a major role in the activation of
CC mature T-cells, and in the thymic differentiation process that leads to
CC CD8 expression. CD8 is expressed either as a homodimer (containing two
CC alpha chains) or as a heterodimer (an alpha and a beta chain). The CD8
CC CD82-like region is involved in regulating T-cell activation. The
CC antagonists of the invention comprise a molecular surface similar to at
CC least a portion of human CD8 molecule surface around the site of one of
CC these peptides. The compounds of the invention compete with CD8 so as to
CC inhibit T-cell activation. They can also be used to treat an individual
CC who is about to undergo, is undergoing, or has undergone a
CC transplantation procedure such as bone marrow, liver, heart, kidney,
CC lung, islets, or cornea transplantation, or skin grafts. The compounds
CC can also be used to treat an individual suspected of suffering from, or
CC susceptible to graft versus host disease.

SO Sequence 8 AA:

Query Match 66.7%; Score 40; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEGDPTOR 9
| | | | | | | |
DB 1 AEGDPTOR 8

RESULT 4
AAAY43646
ID AAY43646 standard; peptide: 8 AA.

XX AAY43646;
XX
DT 11-FEB-2000 (first entry)

DE Fragment of a human CD8 antagonist peptide.

XX Extracellular domain; alpha chain; human CD8; T cell activation;
KM cytotoxic T lymphocyte activation; CTL activation;

KM graft versus host disease; CD8 antagonist; transplant;
KM allogeneic bone marrow transplant.

XX Homo sapiens.

OS
XX
PN WO954345-A1.

PD 28-OCT-1999.

XX 21-APR-1999; 99WO-US08814.

XX 21-APR-1998; 98US-0082436.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Korgold R, Huang Z, Choksi S;

DR WPI; 2000-013224/01.

XX Novel CD8 antagonists used to inhibit cytotoxic T lymphocytes and
PT prevent immune responses -

XX Disclosure; Page 48; 67pp; English.

XX The present sequence represents a fragment of a human CD8 antagonist
CC peptide. The specification describes peptides that are CD8 antagonists,
CC and that compete with regions within the extracellular domain of the
CC alpha chain of CD8 regions in intermolecular interactions that involve
CC CD8 which are associated with cytotoxic T lymphocyte (CTL) activation.
CC These peptides comprise a molecular surface that corresponds to a
CC molecular surface of human CD8 at amino acids 73-76, 38-46, 53-56,
CC 60-67 or 53-67. The peptides can be used in methods and compositions
CC for therapeutically or prophylactically treating graft versus host
CC disease in patients who have or about to undergo transplants, e.g.
CC allogeneic bone marrow transplants. The methods and compositions are
CC also used to treat individuals who are undergoing and/or who have
CC undergone transplants, e.g. transplants of heart, liver, lung, islets
CC or cornea, and skin grafts. The methods are also used to inhibit T cell
CC activation in humans.

XX Sequence 8 AA:

Query Match 66.7%; Score 40; DB 21; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEGDPTOR 9
| | | | | | | |
DB 1 AEGDPTOR 8

RESULT 5
AAR98509
ID AAR98509 standard; peptide: 10 AA.

XX AAR98509;

XX 04-MAR-1997 (first entry)

XX CD8 antagonist #4.

XX CD8 antagonist; inhibitor; T-cell activation; human; CD8 alpha chain;
KM thymic differentiation; transplantation; bone marrow; liver; heart; lung;
KM kidney; cornea; skin graft; graft versus host disease; therapy.

XX Synthetic.

XX WO9622106-A1.

XX 25-JUL-1996.

XX 17-JAN-1996; 96WO-US00310.

XX 17-JAN-1995; 95US-0372952.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Choksi S, Huang Z, Jameson BA, Korgold R;

DR WPI; 1996-354307/35.

XX CD8 antagonist peptide(s) - used for inhibiting T cell activation,
PT partic. for treating transplant rejection or graft versus host
PT disease

XX Claim 16; Page 29; 44pp; English.

XX AAR98506-R98511 represent CD8 antagonists of the invention. CD8 plays a
CC major role in the activation of mature T-cells, and in the thymic
CC differentiation process that leads to CD8 expression. CD8 is expressed
CC either as a homodimer (containing two alpha chains) or as a heterodimer
CC (an alpha and a beta chain). The CD8 CDR2-like region is involved in
CC regulating T-cell activation. The antagonists of the invention comprise
CC a molecular surface similar to at least a portion of human CD8 molecular
CC surface around the site of one of these peptides. The compounds of the
CC invention compete with CD8 so as to inhibit T-cell activation. They can
CC also be used to treat an individual who is about to undergo, is
CC undergoing, or has undergone a transplantation procedure such as bone
CC marrow, liver, heart, kidney, lung, islets, or cornea transplantation,
CC or skin grafts. The compounds can also be used to treat an individual
CC suspected of suffering from, or susceptible to graft versus host
CC disease.

XX Sequence 10 AA:

Query Match 66.7%; Score 40; DB 17; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEGDPTOR 9
| | | | | | | |
DB 2 AEGDPTOR 9

RESULT 6

AAAY43649
ID AAY43649 standard; peptide: 10 AA.

XX AAY43649;

XX 11-FEB-2000 (first entry)

XX Amino acid sequence of a human CD8 antagonist peptide.

```

KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
XX Homo sapiens.
XX
OS Wo200147944-A2.
PN
XX
XX Mo200147944-A2.
PD
XX
XX 05-JUL-2001.
PE
XX 28-DEC-2000; 2000WO-US5498.
PR
XX 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
PI
XX Shinkets RA, Leach M;
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Disclosure; Page 3864; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms.
XX
SQ Sequence 11 AA;
XX
Query Match 53.3%; Score 32; DB 22; Length 11;
Best Local Similarity 75.0%; Pred.No. 7.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0
QY 2 AESIDTOR 9
Db 1 : |||||
3 ARGVDTOR 10
RESULT 8
ABG60421
ID ABG60421 standard; Peptide; 9 AA.
AC
XX ABG60421:
XX
DT 30-JUL-2002 (first entry)
XX
DE Selective targeting peptide #96.
XX
KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
KW inflammation; macular degeneration; anti-inflammatory; antidiabetic;
KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
KW gene therapy.
XX
XX Synthetic.
XX

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PN WO200220769-A1.
XX
PD 14-MAR-2002.
XX
PF 07-SEP-2001; 2001WO-US27692.
XX
PR 08-SEP-2000; 2000US-231266P.
PR 17-JAN-2001; 2001US-0765101.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Arap W, Pasqualini R;
XX
DR MPI; 2002-415731/44.
XX
PT Targeting peptides identified by phage display, useful for targeting
PT delivery to an organ or tissue, particularly for treating a disease,
PT e.g. cancer, inflammatory or autoimmune diseases, infections or
PT cardiovascular disease.
XX
PS Claim 22: Page 89; 317pp; English.
XX
CC The invention relates to an isolated peptide of 100 amino acids or less
CC in size useful for targeting delivery to an organ or tissue, particularly
CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
CC infection, cardiovascular disease or degenerative disease. The peptide is
CC also useful for inducing apoptosis, particularly to a subject with
CC ischememia, cancer, arthritis, diabetes, cardiovascular disease,
CC inflammation or macular degeneration. Furthermore, the peptide is useful
CC for diagnosing the diseases cited above. Targeting peptides of the
CC invention can also be used to deliver an agent to a foetus, by attaching
CC a peptide to the agent and administering the peptide to a pregnant
CC subject. Sequences ABG60326-ABG60574 represent selective targeting
CC peptides of the invention.
XX
SQ Sequence 9 AA:
XX
Query Match 43.3%; Score 26; DB 23; Length 9;
Best Local Similarity 75.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 GLDTQRFS 11
DB 1 GLDTYRGS 8
XX
RESULT 9
ABR78736
ID ABR78736 standard; Peptide: 11 AA.
XX
AC ABR78736;
XX
DT 22-JUL-2002 (first entry)
XX
DE Chicken calyntenin-1 internal peptide SEQ ID NO:13.
XX
KW Human; calyntenin-1; calyntenin-2; calyntenin-3; nervous system;
KW calcium binding protein; neuroprotective; antiinflammatory; nootropic;
KW anticonvulsant; cerebroprotective; cytosolic; ophthalmological; tumour;
KW analgesic; neuroleptic; vaccine; gene therapy; nervous system disorder;
KW metastasis; ARP2/3 complex; neovascularogenesis; neurodegenerative disease;
KW neuroinflammatory disease; epileptic seizure; retinal disease;
KW pathological pain syndrome; psychiatric disorder.
XX
OS Gallus gallus.
XX
PN WO200222819-A2.
XX
PD 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-1B01662.
XX

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PR 14-SEP-2000; 2000EP-0810830.
XX
PA (UY2U-) UNIV ZUERICH.
XX
PI Sonderegger P, Hintsch G, Kinter J, Meskenaitė V, Schrimpf S;
PI Vogt L, Zurlinden A;
XX
DR MPI; 2002-401904/43.
XX
PT Isolated nervous system calcium binding protein, selected from
PT calyntenin-1-3, useful as valuable agents for the treatment of
PT disorders of nervous system and in the development of drugs.
XX
PS Example 2; Page 52; 158pp; English.
XX
CC The present invention describes an isolated nervous system calcium
CC binding protein (I), selected from calyntenin-1, calyntenin-2 or
CC calyntenin-3, used as a pharmaceutical, having calcium binding activity
CC and/or capable of binding ARP2/3 complex. (I) has neuroprotective,
CC antiinflammatory, nootropic, anticonvulsant, cerebroprotective,
CC cytosolic, ophthalmological, analgesic and neuroleptic activities. (I)
CC and the polynucleotide encoding it (II) can be used in vaccines and in
CC gene therapy. (I) and (II) are useful for the screening and for the
CC preparation of a medicament for the treatment of disorders, in particular
CC disorders of nervous system, particularly central nervous system
CC including brain. (I) and (II) are also useful for the preparation of a
CC medicament for the treatment of tumours including prevention or reduction
CC of growth, expansion infiltration and metastasis of primary and
CC metastatic tumours, in particular brain tumour or tumours of retina,
CC where the tumours involve an enhanced activity of ARP2/3 complex or
CC protease functionally connected with (I), in their growth, expansion,
CC infiltration, metastasis and promotion of blood vessels or
CC neovascularogenesis. (I) and (II) are also useful for treating, preventing or
CC ameliorating negative effects of neurodegenerative diseases or
CC neuroinflammatory diseases or epileptic seizures, and for treating,
CC ameliorating or preventing retinal diseases, pathological pain syndromes,
CC psychiatric disorders, learning and memory functions in healthy persons,
CC and for treating tumours. The present sequence represents a chicken
CC calyntenin-1 peptide, which is used in an example from the present
CC invention.
XX
SQ Sequence 11 AA:
XX
Query Match 43.3%; Score 26; DB 23; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 3 EGLDQREFSG 12
DB 1 EGLDQIADG 10
XX
RESULT 10
AAW49400
ID AAW49400 standard; peptide: 9 AA.
XX
AC AAW49400;
XX
DT 05-JUN-1998 (first entry)
XX
DE Human leucocyte antigen DQ4 binding peptide #291.
XX
KW Human leucocyte antigen; HLA-DQ4; combinatorial library;
KW autoimmune disease; chronic articular rheumatism.
XX
OS Synthetic.
XX
PN JP08151396-A.
XX
PD 11-JUN-1996.
XX
PF 28-NOV-1994; 94JP-0292657.
XX

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PR 28-NOV-1994; 94JP-0292657.
 XX
 PA (TEIJ) TEIJIN LTD.
 XX
 DR WPI; 1996-329479/33.
 XX
 PT HLA-binding oligopeptide and an immuno:regulator contg 1c - used in
 PT the treatment of auto:immune disease
 XX
 PS Claim 4; Page 36; 61pp; Japanese.
 XX
 CC This peptide is an example of a peptide which binds to a human leucocyte
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid
 CC combinatorial library comprising the sequence AAV05953, by screening
 CC with an HLA-DQ4 molecule. The peptide is used for the treatment of
 CC autoimmune disease, or especially for treatment of viral diseases.
 XX
 SQ Sequence 9 AA;
 Query Match 41.7%; Score 25; DB 17; Length 9;
 Best Local Similarity 71.4%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 3 EGDLPQR 9
 DB 3 EGDLPQR 9
 RESULT 11
 AA015769
 ID AA015769 standard; Peptide; 11 AA.
 XX
 AC AA015769;
 XX
 DT 31-OCT-1997 (first entry)
 XX
 DE Anion exchange standard peptide.
 XX
 KW Coiled-coil heterodimer; fusion protein; purification; detection;
 KW coil peptide; peptide 0994; affinity chromatography;
 KW anion exchange.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal Ac"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 FT
 FT
 XX
 PN WO9712988-A1.
 XX
 PD 10-APR-1997.
 XX
 PE 04-OCT-1996; 96WO-US16032.
 XX
 PR 06-OCT-1995; 95US-0540397.
 XX
 PA (PENEC-) PENEC.
 XX
 PI Bautista D, Cachia PJ, Hodges RS, Houston ME, Irwin RT;
 PI Tripet B, Yu L;
 XX
 DR WPI; 1997-226231/20.
 XX
 PT Nucleic acid segment encoding one subunit of a coiled dimer protein
 PT - also derived fusion proteins that can be detected or purified by
 PT reaction with the complementary second subunit
 XX
 PS Example 8; Page 36; 80pp; English.
 XX
 CC This peptide sequence comprises an anion exchange standard that
 CC has a net charge at pH 6.0 of -4. The peptide was used in

CC experiments to determine conditions for removal of non-specific
 CC peptides from a selective dimethylammonium affinity column carrying
 CC coil peptide 0994 (see AA015767). It was eluted from the column
 CC by washing with a solution of 1.0 M KCl/10 mM phosphate for 5 min.
 CC Peptide 0994 is used in methods for the detection and purification
 CC of expressed proteins via alpha-helical coiled-coil heterodimer
 CC formation.
 XX
 SQ Sequence 11 AA;
 Query Match 41.7%; Score 25; DB 18; Length 11;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAEGLD 6
 DB 6 AAEGLD 11
 RESULT 12
 AA003264
 ID AA003264 standard; Peptide; 11 AA.
 XX
 AC AA003264;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Fruit fly G protein coupled receptors, DmGPCR6aL/DL ligand #13.
 XX
 KW Fruit fly; G protein coupled receptor; DmGPCR6aL/DL;
 KW human immunodeficiency virus; HIV; cancer; Parkinson's disease;
 KW diabetes; obesity; atherosclerosis; thrombosis; stroke; renal failure;
 KW inflammation; rheumatoid arthritis; autoimmune disorder;
 KW neurological disorder; schizophrenia; manic depression; dementia;
 KW severe mental retardation; dyskinesia; Huntington's disease;
 KW Tourette's syndrome; ligand.
 XX
 OS Drosophila melanogaster.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /note= "C-terminus is amidated"
 FT
 FT
 XX
 PN WO200131005-A2.
 XX
 PD 03-MAY-2001.
 XX
 PE 20-OCT-2000; 2000WO-US29002.
 XX
 PR 22-OCT-1999; 99US-0425676.
 XX
 PA (PHNA) PHARMACIA & UPJOHN CO.
 XX
 PI Lowery DE, Smith VG, Kubiak TA, Larsen MJ;
 PI WPI; 2001-316333/33.
 XX
 DR New Drosophila melanogaster GPCR nucleic acids and polypeptide useful
 DR for inducing an immune response, for identifying homologs and for
 DR treating e.g. diabetes, obesity and manic depression -
 XX
 PS Example 9; Page 99; 110pp; English.
 XX
 CC The sequence is a fruit fly G protein coupled receptors, DmGPCR6aL/DL,
 CC peptide ligand. The proteins are useful for inducing an immune response
 CC against itself in a mammal. The nucleic acids are useful for identifying
 CC an animal homolog of DmGPCR, by screening databases or libraries. The
 CC compounds identified as binding partners or modulators of GPCR binding
 CC are useful for treating diseases in animals, and for control insects that
 CC are harmful or cause injury to plants or animals. Diseases treated
 CC include infections (e.g. viral and human immunodeficiency virus, HIV),
 CC cancer, pain, Parkinson's disease, hypotension, hypertension, diabetes,
 CC obesity, atherosclerosis, thrombosis, stroke, renal failure,

CC inflammation, rheumatoid arthritis, autoimmune disorders, and psychotic
 CC and neurological disorders (anxiety, schizophrenia, manic depression,
 CC delirium, dementia, severe mental retardation, dyskinesias, Huntington's
 CC disease or Tourette's syndrome). The nucleic acids can be used for
 CC genetic mapping, and producing the GPCRs. Anti-GPCR antibodies can be
 CC used in therapy, diagnostic assays and for modulating GPCR activity.

XX Sequence 11 AA:

Query Match 41.7%; Score 25; DB 22; Length 11;
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AEGDITQRF 10
 | | | | |
 Db 2 AEEPLGTRMF 11

RESULT 13

AAU03828 standard; Peptide: 11 AA.

AC AAU03828;

DT 12-SEP-2001 (first entry)

DE G protein-coupled receptor-like (GPCR-like) receptor binding peptide #5.

XX G protein-coupled receptor-like receptor: GPCR-like receptor: helminth;

KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;

KM neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;

KM fruitfly.

XX Caenorhabditis elegans.

OS W0200138533-A2.

PN 31-MAY-2001.

XX 24-NOV-2000; 2000MO-US32225.

XX 24-NOV-1999; 99US-0167523.

XX (PMAA) PHARMACIA & UPJOHN.

PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;

XX WPI; 2001-343952/36.

DR Using G-protein-coupled receptor (GPCR)-like receptors to identify

XX candidate compounds for the treatment and prevention of invertebrate

PT parasites, especially helminths and insects -

XX Claim 18; Page 58; 219pp; English.

XX The sequence represents a G protein-coupled receptor-like (GPCR-like)

CC receptor protein. GPCR-like receptors and their associated nucleic acids

CC may be used to identify candidate compounds for their ability to modulate

CC the activity of GPCRs. The sequences therefore are useful for treating

CC and preventing infection by endoparasitic and ectoparasitic invertebrate

CC parasites, especially helminths and insects, and particularly ailments

CC related to aberrant neurological and neuromuscular function.

XX Sequence 11 AA:

Query Match 41.7%; Score 25; DB 22; Length 11;
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AEGDITQRF 10
 | | | | |
 Db 2 AEEPLGTRMF 11

RESULT 14

AA66812 standard; Peptide: 12 AA.

AC AA66812;

DT 11-SEP-1995 (first entry)

DE Syndecan heparan-attachment sequence used for fusion protein.

KW Cell surface; proteoglycan; syndecan; mouse; mammary; epithelial cell;

KW ectodomain; NMuMG; glycosylation; heparan sulphate; chondroitin sulphate;

KW chimera; chimaeric molecule; effector molecule; receptor; drug;

KW antibody; diagnostic agent.

OS Mus musculus.

PN W09500633-A.

PD 05-JAN-1995.

PF 17-JUN-1994; 94MO-US06920.

PR 17-JUN-1993; 93US-0078683.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Bernfield M, Kato M, Saunders S;

XX WPI; 1995-052071/07.

DR DNA and protein sequences for recombinant syndecan-derived

PT proteoglycans - comprising a core protein having glycosylation

PT sites for heparan sulphate glycosaminoglycan side chains.

XX Claim 25; Page 84; 97pp; English.

XX An example of a heparan sulphate attachment site derived from syndecan

CC proteins, used in the construction of a fusion protein. The sequence is

CC based on the generic attachment site (AA66811) derived from amino acid

CC sequence comparisons between mouse, rat, hamster and human homologs of

CC the syndecan-1 protein sequence. The glycosylation site is found in the

CC extracellular domain of the protein. The fusion protein contains the

CC heparan attachment site, a further chondroitin sulphate

CC glycosaminoglycan group linked to biological effector molecules, cell

CC surface receptors, drugs, antibodies, diagnostic agents or components of

CC microorganisms.

XX Sequence 12 AA:

Query Match 41.7%; Score 25; DB 16; Length 12;
 Best Local Similarity 55.6%; Pred. No. 2.4e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GLDTRFSG 12
 | | | | |
 Db 2 GDDSDNMSG 10

RESULT 15

AA61860 standard; Peptide: 9 AA.

AC AA61860;

DT 18-MAY-1995 (first entry)

DE MBP peptide 108, potential binder of HLA-A2.1.

XX antigen; epitope; immunogenic target protein; PSA; HBVC; HBVS; EBV;

KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;

KW human immunodeficiency virus; human papilloma virus; p53; c-erbB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
 KW algorithm prediction; MBP.
 XX
 OS Homo sapiens.
 XX
 PN W09420127-A.
 XX
 PD 15-SEP-1994.
 XX
 PE 04-MAR-1994; 94WO-US02353.
 XX
 PR 05-MAR-1993; 93US-0027146.
 PR 04-JUN-1993; 93US-0073205.
 PR 29-NOV-1993; 93US-0159184.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Grey HM, Kast WM, Sette A, Sidney J;
 XX
 DR WPI: 1994-302678/37.
 XX
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.
 XX
 PS Disclosure: Page 122; 138pp; English.
 XX
 CC AAR61714-837 are potential peptide binders of HLA-A2.1 motif. These
 CC peptides are thus potentially immunogenic. They were predicted by
 CC using an algorithm, which assigns a score for each amino acid, at
 CC each position along a peptide. A peptide is scored in the 'Grouped
 CC Ratio' algorithm as a product of the scores of each of its residues.
 CC This peptide has an algorithm score (E02) of -23.34. This value can
 CC then be used to predict a population of peptides with the highest
 CC occurrence of good binders. The peptides of the invention can induce
 CC cytotoxic T lymphocytes which can react with target cells. They can
 CC be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 CC
 XX
 SQ Sequence 9 AA;
 Query Match 40.0%; Score 24; DB 15; Length 9;
 Best Local Similarity 62.5%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GLDTRFS 11
 | | | | |
 Db 1 GLSISRFS 8

Search completed: April 15, 2003, 10:20:06
 Job time : 36 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 10:21:05 ; Search time 14 Seconds

(without alignments)

52.402 Million cell updates/sec

Title: US-09-521-527c-1

Perfect score: 60

Sequence: 1 AAEGLDTRFSG 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 34263

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
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12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	36.7	8	US-10-079-625-33	Sequence 33, Appl
2	22	36.7	9	US-09-753-831-10	Sequence 10, Appl
3	22	36.7	9	US-09-753-831-28	Sequence 28, Appl
4	22	36.7	10	US-09-920-174-35	Sequence 35, Appl
5	21	35.0	5	US-09-859-214-18	Sequence 18, Appl
6	21	35.0	5	US-09-859-214-19	Sequence 19, Appl
7	21	35.0	6	US-08-875-849C-14	Sequence 14, Appl
8	21	35.0	6	US-10-213-539-1	Sequence 1, Appl
9	21	35.0	6	US-09-859-214-13	Sequence 13, Appl
10	21	35.0	6	US-09-859-214-15	Sequence 15, Appl
11	21	35.0	6	US-09-859-214-17	Sequence 17, Appl
12	21	35.0	7	US-09-859-214-9	Sequence 9, Appl
13	21	35.0	7	US-09-859-214-12	Sequence 12, Appl
14	21	35.0	7	US-09-859-214-14	Sequence 14, Appl
15	21	35.0	7	US-09-859-214-16	Sequence 16, Appl
16	21	35.0	8	US-09-859-214-58	Sequence 58, Appl
17	21	35.0	9	US-09-859-214-11	Sequence 11, Appl
18	21	35.0	10	US-09-834-765-82	Sequence 82, Appl
19	21	35.0	10	US-09-824-206-5	Sequence 5, Appl

20	21	35.0	10	US-09-859-214-55	Sequence 55, Appl
21	21	35.0	10	US-09-859-214-59	Sequence 59, Appl
22	21	35.0	10	US-09-147-490-1	Sequence 1, Appl
23	21	35.0	10	US-09-779-308-37	Sequence 37, Appl
24	21	35.0	11	US-09-950-313-38	Sequence 30, Appl
25	21	35.0	12	US-09-826-290-82	Sequence 82, Appl
26	21	35.0	12	US-09-859-214-56	Sequence 56, Appl
27	21	35.0	12	US-09-859-214-60	Sequence 60, Appl
28	21	35.0	12	US-10-090-624-22	Sequence 22, Appl
29	21	35.0	12	US-10-052-798-14	Sequence 14, Appl
30	20	33.3	7	US-09-281-495-25	Sequence 25, Appl
31	20	33.3	8	US-09-984-056-54	Sequence 54, Appl
32	20	33.3	8	US-09-984-057-54	Sequence 54, Appl
33	20	33.3	9	US-09-931-325A-156	Sequence 156, App
34	19	31.7	6	US-09-867-852-133	Sequence 133, App
35	19	31.7	7	US-09-832-723-11	Sequence 11, Appl
36	19	31.7	8	US-10-014-485A-53	Sequence 53, Appl
37	19	31.7	8	US-09-910-033A-6	Sequence 6, Appl
38	19	31.7	9	US-10-102-283-119	Sequence 119, App
39	19	31.7	9	US-10-102-283-138	Sequence 138, App
40	19	31.7	9	US-10-091-135-11	Sequence 11, Appl
41	19	31.7	9	US-10-125-635A-85	Sequence 85, Appl
42	19	31.7	9	US-10-125-635A-235	Sequence 235, App
43	19	31.7	9	US-10-125-635A-302	Sequence 302, App
44	19	31.7	9	US-09-931-325A-157	Sequence 157, App
45	19	31.7	9	US-09-834-765-450	Sequence 450, App

ALIGNMENTS

RESULT 1
US-10-079-625-33
Sequence 33, Application US/10079625
Publication No. US20020182676A1
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
City: Boston
STATE: MA
COUNTRY: US
Zip: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTESTO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/079, 625
FILING DATE: 2002-FEB-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkiojohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-079-625-33

Query Match 36.7%; Score 22; DB 9; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AEGIDTOR 9
DB 1 AQCINFOR 8

RESULT 2
US-09-753-831-10
Sequence 10, Application US/09753831
Patent No. US20020137683A1
GENERAL INFORMATION:
APPLICANT: Hogan, Kevin T.
TITLE OF INVENTION: C-SKI Oncogene-Derived Peptides for Prevention,
FILE REFERENCE: 26747-27
CURRENT APPLICATION NUMBER: US/09/753,831
CURRENT FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: U.S. 60/174296
PRIOR FILING DATE: 2000-01-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 9
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. US20020137683A1apeptide
US-09-753-831-10

Query Match 36.7%; Score 22; DB 10; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.2e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GLDTQ 8
DB 5 GLDTK 9

RESULT 3
US-09-753-831-28
Sequence 28, Application US/09753831
Patent No. US20020137683A1
GENERAL INFORMATION:
APPLICANT: Hogan, Kevin T.
APPLICANT: Ross, Mark M.
TITLE OF INVENTION: C-SKI Oncogene-Derived Peptides for Prevention,
TITLE OF INVENTION: Treatment and Diagnosis of Cancer

FILE REFERENCE: 26747-27
CURRENT APPLICATION NUMBER: US/09/753,831
CURRENT FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: U.S. 60/174296
PRIOR FILING DATE: 2000-01-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 9
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. US20020137683A1apeptide
US-09-753-831-28

Query Match 36.7%; Score 22; DB 10; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.2e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GLDTQ 8
DB 5 GLDTK 9

RESULT 4
US-09-920-174-35
Sequence 35, Application US/09920174
Patent No. US20020150590A1
GENERAL INFORMATION:
APPLICANT: KHANNA, RAJIV
APPLICANT: KERR, BEVERLEY M.
APPLICANT: MISKO, THOR S.
APPLICANT: MOSS, DENIS J.
APPLICANT: BURROWS, SCOTT R.
TITLE OF INVENTION: EBV CTL EPITOPES
FILE REFERENCE: FBRC:008USC2
CURRENT APPLICATION NUMBER: US/09/920,174
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 09/920,175
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 09/194,450
PRIOR FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 10
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-920-174-35

Query Match 36.7%; Score 22; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 LDTQRFSG 12
DB 2 LDFVRFMG 9

RESULT 5
US-09-859-214-18
Sequence 18, Application US/09859214
Patent No. US20020103111A1
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MAGCAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 89

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Millitia Drive
;; CITY: Lexington
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02421
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/859,214
;; FILING DATE: 16-May-2001
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/109,879
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/582,740
;; FILING DATE: 04-JAN-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brook, David E.
;; REGISTRATION NUMBER: 22,592
;; REFERENCE/DOCKET NUMBER: LKS95-12A2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (781) 861-6240
;; TELEFAX: (781) 861-9540
;;
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /label= modified aa
;; /note= "Ac - Glycine"
;;
;; NAME/KEY: Modified-site
;; LOCATION: 5
;; OTHER INFORMATION: /label= modified aa
;; /note= "Serine - NH2"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-859-214-18
Query Match 35.0%; Score 21; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GLDT 7
Db 1 GLDT 4
RESULT 6
US-09-859-214-19
; Sequence 19, Application US/09859214
; Patent No. US2002010311A1
; GENERAL INFORMATION:
; APPLICANT: Schwender, Charles F.
; Shroff, Hitesh N.
; TITLE OF INVENTION: INHIBITORS OF MADCAM-1-MEDIATED
; INTERACTIONS AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA

;; ZIP: 02421
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/859,214
;; FILING DATE: 16-May-2001
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/109,879
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/582,740
;; FILING DATE: 04-JAN-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brook, David E.
;; REGISTRATION NUMBER: 22,592
;; REFERENCE/DOCKET NUMBER: LKS95-12A2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (781) 861-6240
;; TELEFAX: (781) 861-9540
;;
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /label= modified aa
;; /note= "Ac - Arginine"
;;
;; NAME/KEY: Modified-site
;; LOCATION: 5
;; OTHER INFORMATION: /label= modified aa
;; /note= "Threonine - NH2"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-859-214-19
Query Match 35.0%; Score 21; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GLDT 7
Db 2 GLDT 5
RESULT 7
US-08-875-849C-14
; Sequence 14, Application US/08875849C
; Patent No. US2002014731A1
; GENERAL INFORMATION:
; APPLICANT: Briskin, Michael J.
; Ringler, Douglas J.
; Picarello, Dominic
; Newman, Walter
; TITLE OF INVENTION: Mucosal Vascular Addressins and Uses
; Thereof
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 530 Virginia Road, PO Box 9133
; CITY: Concord
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 01742-9133
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,849C
FILING DATE: 08-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCJ/US96/02153
FILING DATE: 12-FEB-1996
APPLICATION NUMBER: US 08/523,004
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-04A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 978-341-0036
TELEFAX: 978-341-0136
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-875-849c-14

Query Match 35.0%; Score 21; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GLDT 7
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Db 1 GLDT 4

RESULT 8
US-10-213-539-1
Sequence 1, Application US/10213539
Publication No. US20030003108A1
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Hillan, Kenneth J.
TITLE OF INVENTION: Diagnosis and Treatment of Hepatic Disorders
FILE REFERENCE: P1081R1
CURRENT APPLICATION NUMBER: US/10/213,539
CURRENT FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: US/09/310,247
PRIOR FILING DATE: 1999-05-12
PRIOR APPLICATION NUMBER: US 60/085,326
PRIOR FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 6
TYPE: PRT
ORGANISM: Homo sapiens
US-10-213-539-1

Query Match 35.0%; Score 21; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GLDT 7
| | | |
Db 1 GLDT 4

RESULT 9
US-09-859-214-13
Sequence 13, Application US/09859214
Patent No. US20020103111A1
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.

Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MAGCAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,214
FILING DATE: 16-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/109,879
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/582,740
FILING DATE: 04-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Modified aa
/note= "Ac - tryptophan"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= Modified aa
/note= "threonine - NH2"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-859-214-13

Query Match 35.0%; Score 21; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GLDT 7
| | | |
Db 3 GLDT 6

RESULT 10
US-09-859-214-15
Sequence 15, Application US/09859214
Patent No. US20020103111A1
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MAGCAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,214
FILING DATE: 16-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/109,879
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12A2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-9540
TELEFAX: (781) 861-6240

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Modified aa
/note= "Ac-Glycine"

FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= Modified aa
/note= "Leucine - NH2"

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-859-214-15

Query Match
Best Local Similarity 35.0%; Score 21; DB 10; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GLDT 7
|||||
Db 1 GLDT 4

RESULT 11
US-09-859-214-17
Sequence 17, Application US/09859214
Patent No. US2002010311A1

GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MADCAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,214
FILING DATE: 16-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/109,879
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12A2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-9540
TELEFAX: (781) 861-6240

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= modified aa
/note= "Ac - Arginine"

FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= modified aa
/note= "Serine - NH2"

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-859-214-17

Query Match
Best Local Similarity 35.0%; Score 21; DB 10; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GLDT 7
|||||
Db 2 GLDT 5

RESULT 12
US-09-859-214-9
Sequence 9, Application US/09859214
Patent No. US2002010311A1

GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MADCAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,214

FILING DATE: 16-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/109,879
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/582,740
FILING DATE: 04-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= modified aa
/note= "Ac - Histidine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /label= Modified aa
/note= "Threonine-NH2"
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-859-214-9

Query Match 35.0%; Score 21; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GLDT 7
Db 4 GLDT 7

RESULT 13
US-09-859-214-12
Sequence 12, Application US/09859214
Patent No. US20020103111A1
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MAGCAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,214
FILING DATE: 16-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/109,879
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/582,740

FILING DATE: 04-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= modified aa
/note= "Ac - tryptophan"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /label= Modified aa
/note= "Serine - NH2"
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-859-214-12

Query Match 35.0%; Score 21; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GLDT 7
Db 3 GLDT 6

RESULT 14
US-09-859-214-14
Sequence 14, Application US/09859214
Patent No. US20020103111A1
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MAGCAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,214
FILING DATE: 16-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/109,879
FILING DATE: 04-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= modified aa
/note= "Ac - Arginine"
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /label= modified aa
/note= "Leucine - NH2"
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-859-214-14

Query Match
Best Local Similarity 35.0%; Score 21; DB 10; Length 7;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GLDT 7
||||
DB 2 GLDT 5

RESULT 15
US-09-859-214-16
Sequence 16, Application US/09859214
Patent No. US2002010311A1
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
Shoof, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MAGCAM-1-MEDIATED
INTERACTIONS AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/859,214
FILING DATE: 16-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/109,879
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/582,740
FILING DATE: 04-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-9540
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= modified aa
/note= "Ac - Tryptophan"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /label= modified aa
/note= "Serine - NH2"
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-859-214-16

Query Match
Best Local Similarity 35.0%; Score 21; DB 10; Length 7;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GLDT 7
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DB 3 GLDT 6

Search completed: April 15, 2003, 10:28:03
Job time : 15 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2003, 10:19:29 ; Search time 14 Seconds
(without alignments)
25.220 Million cell updates/sec

Title: US-09-521-527C-1

Perfect score: 60

Sequence: 1 AAEGDPTQRFSG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 91334

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	66.7	8	1	US-08-372-952-3
2	40	66.7	8	1	US-08-875-309-3
3	40	66.7	8	5	PCT-US96-00310-3
4	40	66.7	10	1	US-08-372-952-6
5	40	66.7	10	4	US-08-875-309-6
6	40	66.7	10	5	PCT-US96-00310-6
7	26	43.3	12	4	US-09-242-435-16
8	23	38.3	8	4	US-09-187-859-1699
9	23	38.3	8	6	5168051-15
10	23	38.3	9	4	US-09-117-860-13
11	23	38.3	9	4	US-09-644-600-82
12	22	36.7	8	2	US-08-599-455B-33
13	22	36.7	8	4	US-09-069-781B-33
14	22	36.7	8	4	US-09-137-132-33
15	22	36.7	8	4	US-08-864-564A-33
16	22	36.7	8	4	US-09-094-410-33
17	22	36.7	12	1	US-08-036-555B-164
18	22	36.7	12	1	US-08-469-569-164
19	22	36.7	12	1	US-08-249-322A-164
20	22	36.7	12	1	US-08-469-526A-164
21	22	36.7	12	2	US-08-734-591A-164
22	22	36.7	12	2	US-08-469-660-164
23	22	36.7	12	2	US-08-466-860-5
24	22	36.7	12	3	US-08-472-040A-5
25	22	36.7	12	4	US-08-470-335-164
26	22	36.7	12	4	US-08-735-021-164
27	22	36.7	12	4	US-08-734-664A-164

28	22	36.7	12	4	US-08-276-776-5	Sequence 5, Appl1
29	22	36.7	12	4	US-08-471-209-5	Sequence 5, Appl1
30	22	36.7	12	4	US-08-470-339-164	Sequence 164, App
31	22	36.7	12	4	US-08-467-602-164	Sequence 164, App
32	22	36.7	12	5	PCT-US94-05083C-160	Sequence 160, App
33	22	36.7	12	5	PCT-US95-06846A-164	Sequence 164, App
34	21	35.0	5	3	US-08-582-740-18	Sequence 18, Appl
35	21	35.0	5	4	US-08-582-740-19	Sequence 19, Appl
36	21	35.0	5	4	US-09-109-879-18	Sequence 18, Appl
37	21	35.0	5	4	US-09-109-879-19	Sequence 19, Appl
38	21	35.0	6	3	US-08-582-740-13	Sequence 13, Appl
39	21	35.0	6	3	US-08-582-740-15	Sequence 15, Appl
40	21	35.0	6	3	US-08-582-740-17	Sequence 17, Appl
41	21	35.0	6	4	US-09-109-879-13	Sequence 13, Appl
42	21	35.0	6	4	US-09-109-879-15	Sequence 15, Appl
43	21	35.0	6	4	US-09-109-879-17	Sequence 17, Appl
44	21	35.0	7	2	US-08-627-173-11	Sequence 11, Appl
45	21	35.0	7	2	US-08-535-882A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-372-952-3
Sequence 3, Application US/08372952

Patent No. 5645837

GENERAL INFORMATION:

APPLICANT: Jameson, Bradford A.

APPLICANT: Choksi, Swati

APPLICANT: Koringold, Robert

TITLE OF INVENTION: CD8 Antagonists

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

ADDRESSEE: No. 5645837ris

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/372,952

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1440

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-372-952-3

Query Match 66.7%; Score 40; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASGLDTR 9
Db 1 ASGLDTR 8

RESULT 2

US-08-875-309-3
Sequence 3, Application US/08875309
Patent No. 6180600

GENERAL INFORMATION:

APPLICANT: Jameson, Bradford A.

APPLICANT: Choksi, Swati

APPLICANT: Korgold, Robert

APPLICANT: Huang, Zimei

TITLE OF INVENTION: CD8 Antagonists

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & NO. 6180600ris

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875.309

FILING DATE: 26-NOV-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00310

FILING DATE: 17-JAN-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/372.952

FILING DATE: 17-JAN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1772

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-875-309-3

Query Match

Best Local Similarity 66.7%; Score 40; DB 4; Length 8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASGLDTR 9

Db 1 ASGLDTR 8

RESULT 3

PCT-US96-00310-3

Sequence 3, Application PC/TUS9600310

GENERAL INFORMATION:

APPLICANT: Jameson, Bradford A.

APPLICANT: Choksi, Swati

APPLICANT: Korgold, Robert

APPLICANT: Huang, Zimei

TITLE OF INVENTION: CD8 Antagonists

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00310

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/372.952

FILING DATE: 17-JAN-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1752

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US96-00310-3

Query Match

Best Local Similarity 66.7%; Score 40; DB 5; Length 8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASGLDTR 9

Db 1 ASGLDTR 8

RESULT 4

US-08-372-952-6

Sequence 6, Application US/08372952

Patent No. 5645837

GENERAL INFORMATION:

APPLICANT: Jameson, Bradford A.

APPLICANT: Choksi, Swati

APPLICANT: Korgold, Robert

TITLE OF INVENTION: CD8 Antagonists

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

STREET: No. 5645837ris

CITY: One Liberty Place, 46th Floor

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/372.952

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-372-952-6

Query Match 66.7%; Score 40; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEGDITOR 9
|||||
DB 2 AEGDITOR 9

RESULT 5
US-08-875-309-6
Sequence 6, Application US/08875309
Patent No. 6180600
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Koringold, Robert
APPLICANT: Huang, Zhiwei
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180600r1s
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875.309
FILING DATE: 26-NOV-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE: 17-JAN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372.952
FILING DATE: 17-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

TOPOLOGY: circular
MOLECULE TYPE: protein
US-08-875-309-6

Query Match 66.7%; Score 40; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEGDITOR 9
|||||
DB 2 AEGDITOR 9

RESULT 6
PCT-US96-00310-6
Sequence 6, Application PC/TUS9600310
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Koringold, Robert
APPLICANT: Huang, Zhiwei
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372.952
FILING DATE: 17-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1752
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: protein
PCT-US96-00310-6

Query Match 66.7%; Score 40; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEGDITOR 9
|||||
DB 2 AEGDITOR 9

RESULT 7
US-09-242-435-16
Sequence 16, Application US/09242435
Patent No. 6461863
GENERAL INFORMATION:
APPLICANT: JARVIS, DONALD L.

;; TITLE OF INVENTION: MODIFYING INSECT CELL GLYCOSYLATION PATHWAYS WITH
;; FILE OF INVENTION: BACULOVIRUS EXPRESSION VECTORS
;; FILE REFERENCE: UMYO:00205
;; CURRENT APPLICATION NUMBER: US/09/242,435
;; CURRENT FILING DATE: 1999-02-16
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 16
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-242-435-16

Query Match 43.3%; Score 26; DB 4; Length 12;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 DTORFSG 12
DB 1 DSRFSG 7

RESULT 8
US-09-187-859-1699
;; Sequence 1699, Application US/09187859A
;; Patent No. 6358920
;; GENERAL INFORMATION:
;; APPLICANT: Blaschuk, Orest W.
;; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
;; FILE REFERENCE: 100086.407C1
;; CURRENT APPLICATION NUMBER: US/09/187,859A
;; CURRENT FILING DATE: 1998-11-06
;; NUMBER OF SEQ ID NOS: 4052
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 1699
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Representative cyclic modulating agent based on
;; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-09-187-859-1699

Query Match 38.3%; Score 23; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.9e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 DTORFSG 12
DB 1 DLRFSG 7

RESULT 9
5168051-15
;; Patent No. 5168051
;; APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
;; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
;; NUMBER OF SEQUENCES: 21
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/389,929
;; FILING DATE: 04-AUG-1989
;; SEQ ID NO:15
;; LENGTH: 8
5168051-15

Query Match 38.3%; Score 23; DB 6; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 LDORFS 11
DB 2 LDRNFS 8

RESULT 10
US-09-117-860-13
;; Sequence 13, Application US/09117860A
;; Patent No. 6338955
;; GENERAL INFORMATION:
;; APPLICANT: OGURI, Suguru
;; APPLICANT: MINOWA, Mari
;; APPLICANT: YOSHIDA, Aruto
;; APPLICANT: TANIGUCHI, Naoyuki
;; TITLE OF INVENTION: NOVEL 1-4 N-ACETYLGLUCOSAMINYLTRANSFERASE AND GENE
;; FILE REFERENCE: 081356/0119
;; CURRENT APPLICATION NUMBER: US/09/117,860A
;; CURRENT FILING DATE: 1998-08-12
;; EARLIER APPLICATION NUMBER: WO PCT/JP97/04546
;; EARLIER FILING DATE: 1997-12-10
;; EARLIER APPLICATION NUMBER: JP 161462/1997
;; EARLIER FILING DATE: 1997-06-18
;; EARLIER APPLICATION NUMBER: JP 332411/1996
;; EARLIER FILING DATE: 1996-12-12
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Bovine
US-09-117-860-13

Query Match 38.3%; Score 23; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 AEGDTR 9
DB 2 SEGDRSK 9

RESULT 11
US-09-644-600-82
;; Sequence 82, Application US/09644600
;; Patent No. 6451500
;; GENERAL INFORMATION:
;; APPLICANT: O'Brien, Timothy J.
;; APPLICANT: Tanimoto, Hirotsuhi
;; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
;; FILE REFERENCE: D6064C1P/D
;; CURRENT APPLICATION NUMBER: US/09/644,600
;; CURRENT FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: 09/421,213
;; PRIOR FILING DATE: 1999-10-20
;; PRIOR APPLICATION NUMBER: 09/027,337
;; PRIOR FILING DATE: 1998-02-20
;; NUMBER OF SEQ ID NOS: 98
;; SEQ ID NO 82
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Residues 220-228 of the TADG-15 protein
US-09-644-600-82

Query Match 38.3%; Score 23; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.9e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AEGIDTOR 10
1 1 1 1
Db 1 ARGVELMRF 9

RESULT 12

US-08-599-455B-33
; Sequence 33, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpeper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkielejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-599-455B-33

Query Match 36.7%; Score 22; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 AEGIDTOR 9
1 1 1 1
Db 1 AAGLNFQK 8

RESULT 13

US-09-069-781B-33
; Sequence 33, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.

; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpeper, Janice A.
; APPLICANT: White, David W.

; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,781B
; FILING DATE: 29-APRIL-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: US 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: US 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: US 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: US 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: US 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: US 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: US 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: US 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkielejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-069-781B-33

Query Match 36.7%; Score 22; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 AEGIDTOR 9
1 1 1 1
Db 1 AAGLNFQK 8

RESULT 14

US-09-137-132-33
; Sequence 33, Application US/09137132
; Patent No. 6380363
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,132
FILING DATE: 18-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-137-132-33

Query Match 36.7%; Score 22; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AEGDTR 9
|:|:|:|:
Db 1 AAGLNF 8

RESULT 15
US-08-864-564A-33
Sequence 33, Application US/08864564A
Patent No. 6395498
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.

APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,564A
FILING DATE: 28-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-864-564A-33

Query Match 36.7%; Score 22; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AEGDTR 9
|:|:|:|:
Db 1 AAGLNF 8

Search completed: April 15, 2003, 10:21:40
Job time : 16 secs


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Matches      8; Conservative      1; Mismatches      3; Indels      0; Gaps      0;
QY      1  AAEGLDTQRFSG 12
      1  :||| ||||
      Db      123  ADDGLDELRFSG 134

RESULT 5
C86091
Chlamydia biosynthesis, pyrroline moiety [Imported] - Escherichia coli (strain O157:H7, s
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: C86091
R:Perin, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:1074935; PMID:11206551
A:Accession: C86091
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-631 <STO>
A:Cross-references: GB:AE005174; NID:912518923; PIDN:AAG59191.1; GSPDB:GN00145; UMG:255
C:Genetics:
A:Gene: thic
C:Superfamily: thiamin biosynthesis protein thic

Query Match      63.3%; Score 38; DB 2; Length 631;
Best Local Similarity 66.7%; Pred. No. 31;
Matches      8; Conservative      1; Mismatches      3; Indels      0; Gaps      0;
QY      1  AAEGLDTQRFSG 12
      1  :||| ||||
      Db      123  ADDGLDELRFSG 134

RESULT 6
H82574
Phage-related protein XE291 [Imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: H82574
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82574
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-252 <STM>
A:Cross-references: GB:AE004041; GB:AE003849; NID:9107453; PIDN:AAF85090.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Molecule type: DNA
A:Status: preliminary
A:Contents: annotation
C:Genetics:
A:Gene: XE291
C:Superfamily:

Query Match      61.7%; Score 37; DB 2; Length 252;
Best Local Similarity 70.0%; Pred. No. 20;
Matches      7; Conservative      1; Mismatches      2; Indels      0; Gaps      0;
QY      1  AAEGLDTQRF 10
      1  :||| |||
      Db      714  AAEGLDTQRF 723

RESULT 7
C82548
Phage-related DNA polymerase XE2525 [Imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: C82548
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: C82548
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-726 <STM>
A:Cross-references: GB:AE004059; GB:AE003849; NID:9107718; PIDN:AAF85323.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; La
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Molecule type: DNA
A:Status: preliminary
A:Contents: annotation
C:Genetics:
A:Gene: XE2525
C:Superfamily: phage SP02 DNA-directed DNA polymerase

Query Match      61.7%; Score 37; DB 2; Length 726;
Best Local Similarity 70.0%; Pred. No. 55;
Matches      7; Conservative      1; Mismatches      2; Indels      0; Gaps      0;
QY      1  AAEGLDTQRF 10
      1  :||| |||
      Db      714  AAEGLDTQRF 723

RESULT 8
H82774
Phage-related DNA polymerase XE0683 [Imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: H82774
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82774
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-726 <STM>
A:Cross-references: GB:AE003912; GB:AE003849; NID:9105560; PIDN:AAF83493.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
```

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Matches      7; Conservative      1; Mismatches      2; Indels      0; Gaps      0;
QY      1  AAEGLDTQRF 10
      1  :||| |||
      Db      240  AAEGLDTQRF 249

RESULT 7
C82548
Phage-related DNA polymerase XE2525 [Imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: C82548
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: C82548
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-726 <STM>
A:Cross-references: GB:AE004059; GB:AE003849; NID:9107718; PIDN:AAF85323.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; La
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Molecule type: DNA
A:Status: preliminary
A:Contents: annotation
C:Genetics:
A:Gene: XE2525
C:Superfamily: phage SP02 DNA-directed DNA polymerase

Query Match      61.7%; Score 37; DB 2; Length 726;
Best Local Similarity 70.0%; Pred. No. 55;
Matches      7; Conservative      1; Mismatches      2; Indels      0; Gaps      0;
QY      1  AAEGLDTQRF 10
      1  :||| |||
      Db      714  AAEGLDTQRF 723

RESULT 8
H82774
Phage-related DNA polymerase XE0683 [Imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: H82774
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82774
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-726 <STM>
A:Cross-references: GB:AE003912; GB:AE003849; NID:9105560; PIDN:AAF83493.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
```

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 A:Author: Martins, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, B
 A:Author: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Author: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Teshko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF0683
 C:Superfamily: phage SPO2 DNA-directed DNA polymerase

Query Match 61.7%; Score 37; DB 2; Length 726;
 Best Local Similarity 70.0%; Pred. No. 53;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAGLDTORF 10
 |||||
 DB 714 AAGGPTTTR 723

RESULT 9

A46546
 Leukocyte common antigen long splice form precursor - human
 N:Alternate names: CD45; protein-tyrosine-phosphatase, receptor type c; T200 glycoprotein
 N:Contents: leukocyte common antigen intermediate splice form; leukocyte common antigen
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
 C:Accession: A46546; B46546; A29449; B29449; I57658
 R:Strull, M.; Hall, L.R.; Sagar, Y.; Schlossman, S.F.; Saito, H.
 J. Exp. Med. 166, 1548-1566, 1987
 A:Title: Differential usage of three exons generates at least five different mRNAs encod
 A:Reference number: A46546; MUID:88061067; PMID:2824653
 A:Accession: A46546
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1304 <STR>
 A:Cross-references: GB:Y00638
 A:Experimental source: clone LCA.6/2
 A:Accession: B46546
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-32,99-264 <ST2>
 A:Cross-references: GB:Y00638
 A:Experimental source: clone LCA.111 and clone LCA.260
 A:Accession: C46546
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-31,193-264 <ST3>
 A:Cross-references: GB:Y00638
 A:Experimental source: clone LCA.1
 R:Ralph, S.J.; Thomas, M.L.; Morton, C.C.; Trowbridge, I.S.
 EMBO J. 6, 1251-1257, 1987
 A:Title: Structural variants of human T200 glycoprotein (leukocyte-common antigen).
 A:Reference number: A91066; MUID:87275816; PMID:2996090
 A:Accession: A29449
 A:Molecule type: mRNA
 A:Residues: 1-31,193-649, 'L', 651-869, 'G', 871-872, 'A', 874-1206, 'P', 1208-1304 <RAL>
 A:Cross-references: GB:Y00662; NID:934275; PIDN:CAA68269.1; PID:934276
 A:Experimental source: clones pHLG-1 and lambdaHLG1
 A:Accession: B29449
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 32-192 <RA2>
 A:Experimental source: clone HLC-2
 R:Tsal, A.Y.; Streuli, M.; Saito, H.
 Mol. Cell. Biol. 9, 4550-4555, 1989
 A:Title: Integrity of the exon 6 sequence is essential for tissue-specific alternative s
 A:Reference number: I57658; MUID:90066468; PMID:2531281
 A:Accession: I57658
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 146-192 <RES>
 A:Cross-references: GB:I29253; NID:9187020; PIDN:AA59497.1; PID:9553521
 C:Genetics:
 A:Gene: GDB:PPRC; CD45
 A:Cross-references: GDB:119768; OMIM:151460
 A:Map position: 1931-1932
 C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain ho
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester
 F:54-1235/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:675-899/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:851/Active site: Cys (phosphotyrosine intermediate) #status predicted
 F:857/Binding site: substrate phosphate (Arg) #status predicted

Query Match 60.0%; Score 36; DB 1; Length 1304;
 Best Local Similarity 77.8%; Pred. No. 15e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GLDPTQRFSG 12
 |||||
 DB 119 GTDPTQFSG 127

RESULT 10

S25663
 T-cell surface glycoprotein CD8 alpha chain - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S25663
 R:Altor, P.; Bucci, C.; Fornaro, M.; Rattazzi, M.C.; Nakauchi, H.; Herzenberg, L.A.;
 Immunology 76, 95-102, 1992
 A:Title: Molecular cloning, reconstruction and expression of the gene encoding the al
 A:Reference number: S25663; MUID:92332098; PMID:1628904
 A:Accession: S25663
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-242 <TAI>
 A:Cross-references: EMBL:X59416; NID:9190; PIDN:CAA42051.1; PID:9191
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: glycoprotein; transmembrane protein

Query Match 58.3%; Score 35; DB 2; Length 242;
 Best Local Similarity 63.6%; Pred. No. 46;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 AEGDPTQRFSG 12
 |||||
 DB 85 AEGDPTQRFSG 95

RESULT 11

AE0154
 Probable nucleoid-associated protein YPO1262 [imported] - Yersinia pestis (strain CO9
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C:Accession: AE0154
 R:Parikh, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
 ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AE0154
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-334 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CA90096.1; PID:915979316; GSPDB:GN00175
 C:Genetics:
 A:Gene: YPO1262

Query Match 58.3%; Score 35; DB 2; Length 334;
 Best Local Similarity 87.5%; Pred. No. 63;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDQ 8
 |||||
 DB 188 AAEGLDTRK 195

RESULT 12

F95953
 probable glycosyltransferase, forming alpha-glycosyl linkages protein expc [imported] -
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Apr-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: F95953
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1,583-kb pSymb megaplasmid from the N2-fixing endo
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: F95953
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-417 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CAC49294.1; PID:915140780; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymb
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 Pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebauly, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: expc: SMB21318
 A:Genome: plasmid

Query Match 58.3%; Score 35; DB 2; Length 417;
 Best Local Similarity 75.0%; Pred. No. 78;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 EAGDQRF 10
 |||||
 DB 188 EGVDRTRF 195

RESULT 13

C81965
 hypothetical periplasmic protein NMA0476 [imported] - Neisseria meningitidis (strain Z24
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: C81965
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,
 ; Holroyd, S.; Jørgensen, K.; Leather, S.; Moutle, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: AB175; MUID:20222556; PMID:10761919
 A:Accession: C81965
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-505 <PAR>
 A:Cross-references: GB:AL162753; GB:AL157959; NID:q7379120; PIDN:CAB83771.1; PID:q737922
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA0476

Query Match 58.3%; Score 35; DB 2; Length 505;
 Best Local Similarity 72.7%; Pred. No. 94;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAEGLDQRFSG 12
 |||||
 DB 184 AAEGLDQRFSG 194

RESULT 14

F87664
 glycine cleavage system P protein, subunit 2 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: F87664
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
 n. J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: AB7249; MUID:21173698; PMID:11259647
 A:Accession: F87664
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-524 <SNO>
 A:Cross-references: GB:AE005673; NID:q13425054; PIDN:AAK25314.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC3352

Query Match 58.3%; Score 35; DB 2; Length 524;
 Best Local Similarity 58.3%; Pred. No. 97;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAEGLDQRFSG 12
 |||||
 DB 479 AAKAGDTRFKG 490

RESULT 15

E70752
 probable dead protein - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Feb-2001
 C:Accession: E70752
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
 ; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
 A:Reference number: A70300; MUID:96295987; PMID:9634230
 A:Accession: E70752
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-563 <COL>
 A:Cross-references: GB:E77137; GB:AL123456; NID:q3261593; PIDN:CAB00899.1; PID:e25488
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: dead
 C:Keywords: ATP; nucleotide binding; P-loop
 F:57-64/Region: nucleotide-binding motif A (P-loop)
 F:159-164/Region: nucleotide-binding motif B
 F:163-166/Region: DEAD motif

Query Match 58.3%; Score 35; DB 2; Length 563;
 Best Local Similarity 63.6%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAEGLDQRF 11
 |||||
 DB 310 AARGLDVERIS 320

Search completed: April 15, 2003, 10:14:47
 Job time : 45 secs

GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 10:11:05 ; Search time 11 Seconds

(without alignments)
45.247 Million cell updates/sec

Title: US-09-521-527C-1

Sequence: 1 AAEGIDTQRFSG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	198	1	CD8A_PONPY
2	60	100.0	235	1	CD8A_HUMAN
3	41	68.3	239	1	CD8A_CANFA
4	38	63.3	631	1	THIC_ECO57
5	38	63.3	631	1	THIC_ECOLI
6	36	60.0	1304	1	CD45_HUMAN
7	35	58.3	242	1	CD8A_BOVIN
8	35	58.3	563	1	DEAD_MYCTU
9	35	58.3	628	1	DEAD_ECOLI
10	35	58.3	631	1	THIC_SALTI
11	35	58.3	631	1	THIC_SALTY
12	35	58.3	642	1	DEAD_KLEPN
13	35	58.3	829	1	GUTR_BACSU
14	35	58.3	1134	1	PHY1_SELMA
15	35	58.3	1515	1	GUTR_AZORB
16	34.5	57.5	290	1	AMPR_CITFR
17	34.5	57.5	290	1	AMPR_ENTCL
18	34	56.7	90	1	YGGX_HAEIN
19	34	56.7	203	1	AROG_AMEYE
20	34	56.7	375	1	INTE_ECOLI
21	34	56.7	380	1	VINT_BPR21
22	34	56.7	552	1	CHOD_BREST
23	34	56.7	693	1	VG50_BPMD2
24	34	56.7	849	1	PHSG_SYNY3
25	34	56.7	1056	1	DPOL_ADE02
26	34	55.8	1056	1	DPOL_ADE05
27	33.5	55.8	706	1	CATE_MYCAV
28	33	55.0	328	1	AFUC_HAEIN
29	33	55.0	372	1	YEF1_ECOLI
30	33	55.0	432	1	DAD1_PSEAE
31	33	55.0	484	1	NTRC_RHIME
32	33	55.0	527	1	PTB_MOUSE
33	33	55.0	531	1	PTB_HUMAN

34	33	55.0	555	1	PTB_RAT	000438	rattus norv
35	33	55.0	601	1	DEAD_BUCAT	P57453	buchnera ap
36	33	55.0	714	1	YEF7_YEAST	P43556	saccharomyc
37	33	55.0	948	1	RCSC_SALTI	O56128	salmonella
38	33	55.0	948	1	RCSC_SALTY	P58662	salmonella
39	33	55.0	1193	1	DPOL_ADE04	P87503	human adeno
40	33	55.0	1195	1	YABE_SCHPO	O09847	human adeno
41	33	55.0	2132	1	PGCA_MOUSE	O01282	schizosacch
42	32.5	54.2	296	1	AMPR_PSEAE	P24734	mus muscicu
43	32.5	54.2	930	1	SM6C_HUMAN	O9h312	pseudomonas
44	32.5	54.2	931	1	SM6C_MOUSE	O9wtm3	homo sapien
45	32.5	54.2	960	1	SM6C_RAT	O9wtl3	mus muscicu
							rattus norv

ALIGNMENTS

RESULT 1
CD8A_PONPY
ID CD8A_PONPY STANDARD; PRT; 198 AA.
AC P30433;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte differentiation antigen T8/LEU-2).
GN CD8A.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI-TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate Jari;
RX MEDLINE=92307742; PubMed=1612644;
RA Lawlor D.A., Parham P.;
RT "Structure of CD8 alpha and beta chains of the orangutan: novel patterns of mRNA splicing encoding hingeless polypeptides.";
RL Immunogenetics 36:121-125(1992).
CC -1- FUNCTION: IDENTIFIES CYTOTOXIC/SUPPRESSOR T-CELLS THAT INTERACT WITH MHC CLASS I BEARING TARGETS. CD8 IS THOUGHT TO PLAY A ROLE IN THE PROCESS OF T-CELL MEDIATED KILLING. CD8 ALPHA CHAINS BINDS TO CLASS I MHC MOLECULES ALPHA-3 DOMAINS.
CC -1- SUBUNIT: IN GENERAL HETERODIMER OF AN ALPHA AND A BETA CHAIN LINKED BY TWO DISULFIDE BONDS. CAN ALSO FORM HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL: X60223; CAA42784.1; -.
CC HSSP: P01732; ICD8.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
KW Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell; Immune response; Signal.
FT SIGNAL 1 21
FT CHAIN 22 198
FT
FT DOMAIN 22 145
FT TRANSMEM 146 166
FT DOMAIN 167 198
FT DOMAIN 22 135
FT DOMAIN 135 115
FT DISULFID 43 115
BY SIMILARITY.
T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
BY SIMILARITY.

SQ SEQUENCE 198 AA: 22099 MW: F3EC093EADB05561 CRC64;
 Query Match 100.0%; Score 60; DB 1; Length 198;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAEGLDTPREFSG 12
 Db 80 AAEGLDTPREFSG 91
 RESULT 2
 CD8A.HUMAN STANDARD: PRT: 235 AA.
 AC P01732;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE T-cell surface glycoprotein CD8 alpha chain precursor (T-Lymphocyte
 differentiation antigen T8/Leu-2).
 GN CD8A OR MAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8509337; PubMed=3871356;
 RA Altman D.R., Thomas Y., Madson P.J., Chess L., Axel R.;
 RT "The isolation and sequence of the gene encoding T8: a molecule
 defining functional classes of T lymphocytes.";
 RL Cell 40:237-246(1985).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86103103; PubMed=3936473;
 RA Parnes J.R., Sizer K.C., Sukhatme V.P., Hunkapiller T.;
 RT "Structure of Leu-2/T8 as deduced from the sequence of a cDNA clone.";
 RL Behring Inst. Mitt. 77:48-55(1985).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85124610; PubMed=3918796;
 RA Sukhatme V.P., Sizer K.C., Vollmer A.C., Hunkapiller T.,
 RA Parnes J.R.;
 RT "The T cell differentiation antigen Leu-2/T8 is homologous to
 immunoglobulin and T cell receptor variable regions.";
 RL Cell 40:591-597(1985).
 RN (4)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90035142; PubMed=2509342;
 RA Nakayama K.-I., Tokito S., Okumura K., Nakachi H.;
 RT "Structure and expression of the gene encoding CD8 alpha chain (Leu-
 2/T8).";
 RL Immunogenetics 30:393-397(1989).
 RN (5)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89215302; PubMed=2496167;
 RA Norment A.M., Lonberg N., Lacy E., Littman D.R.;
 RT "Alternatively spliced mRNA encodes a secreted form of human CD8
 alpha. Characterization of the human CD8 alpha gene.";
 RL J. Immunol. 142:3312-3319(1989).
 RN (6)
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 22-135.
 RX MEDLINE=92191292; PubMed=1547508;
 RA Leahy D.J., Axel R., Hendrickson W.A.;
 RT "Crystal structure of a soluble form of the human T cell coreceptor
 CD8 at 2.6-A resolution.";
 RL Cell 68:1145-1162(1992).
 CC -1- FUNCTION: IDENTIFIES CYTOTOXIC/SUPPRESSOR T-CELLS THAT INTERACT
 WITH MHC CLASS I BEARING TARGETS. CD8 IS THOUGHT TO PLAY A ROLE IN
 THE PROCESS OF T-CELL MEDIATED KILLING. CD8 ALPHA CHAINS BINDS TO
 CLASS I MHC MOLECULES ALPHA-3 DOMAINS.
 CC -1- SUBUNIT: IN GENERAL HETERODIMER OF AN ALPHA AND A BETA CHAIN
 LINKED BY TWO DISULFIDE BONDS. CAN ALSO FORM HOMODIMERS.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: VARIOUS PATTERNS OF DIFFERENTIAL SPLICING
 CC OF CD8 ALPHA TRANSCRIPTS INVOLVE EXCISION OF THE TRANSMEMBRANE OR
 CC CYTOPLASMIC DOMAINS.
 CC -1- PPM: ALL OF THE FIVE MOST CARBOXYL-TERMINAL CYSTEINES ARE USED TO
 CC FORM INTER-CHAIN DISULFIDE BONDS IN DIMERS AND HIGHER MULTIMERS,
 CC WHILE THE FOUR AMINO-TERMINAL CYSTEINES ARE NOT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD8a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd8a1pha.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M26315; AAA79217.1; -
 DR EMBL; M26313; AAA79217.1; JOINED.
 DR EMBL; M26314; AAA79217.1; JOINED.
 DR EMBL; M12824; AAA61133.1; -
 DR EMBL; M12826; AAB04637.1; -
 DR EMBL; M27161; AAA59674.1; -
 DR PIR; A01999; RMHUT8.
 DR PIR; A22824; A22824.
 DR PIR; JP0105; JP0105.
 DR PIR; A30604; A30604.
 DR PIR; A45888; A45888.
 DR PDB; 1CD8; 31-JAN-94.
 DR Genew; HGNC:1706; CD8A.
 DR MIM; 186910; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 KW Immunoglobulin domain; Transmembrane; Glycoprotein; Phosphorylation;
 KW T-cell; Immune response; Signal; 3D-structure; Alternative splicing;
 FT SIGNAL 1 21
 FT CHAIN 22 235
 FT
 FT DOMAIN 22 182
 FT TRANSMEM 183 203
 FT DOMAIN 204 235
 FT DOMAIN 22 135
 FT DISULFID 43 115
 FT STRAND 24 27
 FT TURN 35 36
 FT TURN 39 45
 FT STRAND 34 59
 FT STRAND 68 73
 FT STRAND 79 80
 FT TURN 82 83
 FT TURN 86 88
 FT TURN 89 94
 FT TURN 95 96
 FT STRAND 97 102
 FT HELIX 107 109
 FT STRAND 111 119
 FT TURN 120 121
 FT TURN 122 125
 FT STRAND 129 131
 FT STRAND 129 131
 SQ SEQUENCE 235 AA: 25729 MW: FCCA29BAA73726BB CRC64;
 Query Match 100.0%; Score 60; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 9.4e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AAEGLDTPREFSG 12
 Db 80 AAEGLDTPREFSG 91

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RESULT 3
ID  CDBA_CANFA          STANDARD:          PRT:          239 AA.
AC  P33706;
DT  01-FEB-1994 (Rel. 28, Created)
DE  01-FEB-1994 (Rel. 28, Last sequence update)
DE  15-JUN-2002 (Rel. 41, Last annotation update)
DE  T-cell surface glycoprotein CD8 alpha chain precursor.
GN  CD8A.
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX  NCBI_TaxID=9615;
[1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Beagle; TISSUE=Thymus;
RX  MEDLINE=94378217; PubMed=8091416;
RT  Gorman S.D., Frewin M.R., Cobbold S.P., Waldmann H.;
RT  "Isolation and expression of cDNA encoding the canine CD4 and CD8
RT  alpha antigens."
RL  Tissue Antigens 43:184-188(1994).
CC  -1- FUNCTION: IDENTIFIES CYTOTOXIC/SUPPRESSOR T-CELLS THAT INTERACT
CC  WITH MHC CLASS I BEARING TARGETS. CD8 IS THOUGHT TO PLAY A ROLE IN
CC  THE PROCESS OF T-CELL MEDIATED KILLING. CD8 ALPHA CHAINS BINDS TO
CC  CLASS I MHC MOLECULES ALPHA-3 DOMAINS.
CC  -1- SUBUNIT: IN GENERAL, HETERODIMER OF AN ALPHA AND A BETA CHAIN
CC  LINKED BY TWO DISULFIDE BONDS. CAN ALSO FORM HOMODIMERS.
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC  -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-----
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CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL: L14287; AAB02294.1; -
DR  HSP: P01732; ICDB.
DR  InterPro: IPR003006; Ig_MHC.
DR  InterPro: IPR003596; Ig_V.
DR  Pfam: PF00047; Ig_1.
DR  SMART: SM00406; IGV; 1.
KW  Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW  Immune response; Signal.
FT  SIGNAL 1 21
FT  CHAIN 22 239
FT  DOMAIN 22 186
FT  TRANSMEM 187 210
FT  DOMAIN 211 239
FT  DOMAIN 225 139
FT  DISULFID 46 119
FT  CARBOHYD 156 156
SQ  SEQUENCE 239 AA; 26036 MW; 1018579779A5C87B CRC64;

Query Match
Best Local Similarity 68.3%; Score 41; DB 1; Length 239;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 AEGIDTQRFSG 12
ID 1111111111
DB 84 AEGIDTKHISG 94

RESULT 4
THIC_ECO57
ID THIC_ECO57          STANDARD:          PRT:          631 AA.
AC  Q8X6X9;

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DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thiamine biosynthesis protein thic.
DE THIC OR Z5569 OR ECS4917.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boulton A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lam S., Dimalanta E.T., Potamianos K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Ikeda T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -1- FUNCTION: Required for the synthesis of the hydromethylpyrimidine
CC (HMP) moiety of thiamine (4-amino-2-methyl-5-
CC hydroxymethylpyrimidine) (By similarity).
CC -1- PATHWAY: Thiamine biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE THIC FAMILY.
-----
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-----
DR EMBL: AE005631; AAG59191.1; -
DR EMBL: AP002567; BAB38340.1; -
DR InterPro: IPR002817; Thic.
DR Pfam: PF01964; Thic; 1.
DR ProDom: PD007048; Thic; 1.
DR TIGRFAMs: TIGR00190; thic; 1.
KW Thiamine biosynthesis; Complete proteome.
SQ SEQUENCE 631 AA; 70814 MW; 5494CBB9C036F2E CRC64;

Query Match
Best Local Similarity 63.3%; Score 38; DB 1; Length 631;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 AEGIDTQRFSG 12
ID 1111111111
DB 123 ADDGLDELRFSG 134

RESULT 5
THIC_ECOLI
ID THIC_ECOLI          STANDARD:          PRT:          631 AA.
AC  P30136;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thiamine biosynthesis protein thic.
DE THIC OR B3994.

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OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=93163063; PubMed=8432721;
RA Vander Horn P.B., Backstrom A.D., Stewart V., Begley T.P.;
RT "Structural genes for thiamine biosynthetic enzymes (thiCEGH) in
RT Escherichia coli K-12."
RL J. Bacteriol. 175:982-992(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=94089392; PubMed=8265357;
RA Blatner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA Daniels D.L.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT region from 89.2 to 92.8 minutes."
RL Nucleic Acids Res. 21:5408-5417(1993).
CC -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF THE HYDROMETHYLPYRIMIDINE
CC (HMP) MOIETY OF THIAMINE (4-AMINO-2-METHYL-5-
CC HYDROXYMETHYLPYRIMIDINE).
CC -1- PATHWAY: Thiamine biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE THIC FAMILY.
CC -----
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CC -----
DR EMBL: M88701; AAB5616.1; -
DR EMBL: U00006; AAC43092.1; -
DR EMBL: AE000473; AAC76968.1; -
DR PIR: S5117; S5117.
DR Ecogene: E01585; thic.
DR InterPro: IPR002817; Thic.
DR Pfam: PF01964; thic. 1.
DR ProDom: PD007048; thic. 1.
DR TIGRfam: TIGR00190; thic. 1.
KW Thiamine biosynthesis; Complete proteome.
FT CONFLICT 623 630 EYLKKE -> RNL (IN REF. 1).
SQ SEQUENCE 631 AA; 70850 MW; 6P2105B4792CBA3F CRC64;

Query Match 63.3%; Score 38; DB 1; Length 631;
Best Local Similarity 66.7%; Pred. NO. 7.5;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAEGLDTRFG 12
ID 1 : 1111 1111
DB 123 ADDGLDELRFSG 134

RESULT 5
CD45_HUMAN STANDARD; PRT; 1304 AA.
AC P08575;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (CD45 antigen)
DE (TT200)
GN PTPRC OR CD45.
GS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE-Lymphocytes;
RX MEDLINE=88061067; PubMed=2824653;
RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;
RT "Differential usage of three exons generates at least five different
RT mRNAs encoding human leukocyte common antigens."
RL J. Exp. Med. 166:1548-1566(1987).
RN [2]
RP FUNCTION.
RX MEDLINE=89017162; PubMed=2845400;
RA Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
RT "The leukocyte common antigen (CD45): a putative receptor-linked
RT protein tyrosine phosphatase."
RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
RN [3]
RP MYOGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
RT domains of the receptor-linked protein tyrosine phosphatases LCA and
RT LAR."
RL EMBO J. 9:2399-2407(1990).
CC -1- FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN
CC RECEPTOR. THE FIRST PTPASE DOMAIN HAS ENZYMAIC ACTIVITY, WHILE
CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
CC FIRST ONE.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 8 ISOFORMS ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- PTM: HEAVILY N- AND O-GLYCOSYLATED.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- DATABASE: NAME=PROM; NOTE=CD guide CD45 entry;
CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm.
CC -----
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CC -----
DR EMBL: Y00638; CA68669.1; -
DR HSPP: P18052; IYFO.
DR GlycoSiteDB: P08575; -
DR Genew: HGNC:9666; PTPRC.
DR MIM: 151460; -
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR000367; TYR-phosphatase.
DR InterPro: IPR000242; TYL_PP.
DR Pfam: PF00041; In3; 2.
DR Pfam: PF00102; Y-phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00060; FN3; 2.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS0056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS0055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Phosphorylation; B-cell; T-cell; Repeat;
KW Alternative splicing; Hydrolase; Signal.
FT SIGNAL 1 23
FT CHAIN 24 1304 LEUKOCYTE COMMON ANTIGEN.
FT DOMAIN 24 575 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 576 597 POTENTIAL.
FT DOMAIN 598 1304 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 387 479 FIBRONECTIN TYPE-III 1.
FT DOMAIN 480 571 FIBRONECTIN TYPE-III 2.
FT DOMAIN 670 919 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 961 1235 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 851 851
FT ACT_SITE 1167 1167

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FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN 851 851 C->S: LOSS OF ACTIVITY.
SQ SEQUENCE 1304 AA; 147253 MW; 1F357BC563261882 CRC64;

Query Match
Best Local Similarity 60.0%; Score 36; DB 1; Length 1304;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GJDTQRFSG 12
DB 119 GJDTQRFSG 127

RESULT 7
CD8A_BOVIN STANDARD; PRT; 242 AA.
AC P31783;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T-cell surface glycoprotein CD8 alpha chain precursor.
GN CD8A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=92332098; PubMed=1628904;
RA Lalor P., Buccì C., Fornaro M., Rattazzi M.C., Nakauchi H.,
RA Herzenberg L.A., Alberti S.;
RT "Molecular cloning, reconstruction and expression of the gene
RT encoding the alpha-chain of the bovine CD8 -- definition of three
RT peptide regions conserved across species.";
RL Immunology 76:95-102(1992).
CC -1- FUNCTION: IDENTIFIES CYTOTOXIC/SUPPRESSOR T-CELLS THAT INTERACT
CC WITH MHC CLASS I BEARING TARGETS. CD8 IS THOUGHT TO PLAY A ROLE IN
CC THE PROCESS OF T-CELL MEDIATED KILLING. CD8 ALPHA CHAINS BINDS TO
CC CLASS I MHC MOLECULES ALPHA-3 DOMAINS.
CC -1- SUBUNIT: IN GENERAL, HETERODIMER OF AN ALPHA AND A BETA CHAIN
CC LINKED BY TWO DISULFIDE BONDS. CAN ALSO FORM HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC
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CC -----
CC EMBL: X59416; CAA42051.1; -
CC PIR: S25663; S25663.
CC HSPF: P01732; IC08.
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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW Immune response; Signal.
FT STGNAL 1 25 POTENTIAL.
FT CHAIN 26 242 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA
FT CHAIN.
FT DOMAIN 26 189 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 190 214 POTENTIAL.
FT DOMAIN 215 242 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 140 IG-LIKE V-TYPE DOMAIN.
FT DISULFID 47 120 BY SIMILARITY.
SQ SEQUENCE 242 AA; 26417 MW; 91481320EF05195E CRC64;

Query Match
Best Local Similarity 58.3%; Score 35; DB 1; Length 242;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AEGIDTQRFSG 12
DB 85 AEGIDTQRFSG 95

RESULT 8
DEAD_MYCTU STANDARD; PRT; 563 AA.
AC Q11039;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cold-shock DEAD-box protein A homolog (Arp-dependent RNA helicase dead
DE homology).
GN DEAD OR CSDA OR RY1253 OR MT1292 OR MYC50.29C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skellon S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson R., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikala A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: HAS A HELIX-DESTABILIZING ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
CC -----
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 DR EMBL: 277137; CAB00899.1; -
 DR EMBL: AE007004; AAK45550.1; -
 DR HSSP: 058083; 1HV8.
 DR TIGR: MT1292; -
 DR Tuberculin; RV1253; -
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR000629; DEAD_box.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD.1.
 DR Pfam: PF00271; Helicase_C.1.
 DR SMART: SM00487; DEXDC.1.
 DR SMART: SM00490; HELICG.1.
 DR PROSITE: PS00039; DEAD_ATP_HELICASE.1.
 DR Hydroxylase; Helicase; ATP-binding; RNA-binding;
 KM Transcription regulation; Complete proteome.
 FT NP_BIND 57 64 ATP (BY SIMILARITY).
 FT SITE 163 166 DEAD BOX
 SO SEQUENCE 563 AA; 61452 MW; 5D6D0FAE15D3AEDE CRC64;

 Query Match 58.3%; Score 35; DB 1; Length 563;
 Best Local Similarity 63.6%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 QY 1 AAEGLDTPRFS 11
 DB 310 AARGLDVERIS 320

 RESULT 9
 DEAD_ECOLI STANDARD; PRT; 628 AA.
 AC P23304;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cold-shock DEAD-box protein A (ATP-dependent RNA helicase dead).
 GN DEAD OR CSDA OR MSSB OR B3162.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxId=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91258309; PubMed=2045359;
 RA Toome W.M., Rudd K.E., Priesen J.D.;
 RT "dead, a new Escherichia coli gene encoding a presumed ATP-dependent
 RT RNA helicase, can suppress a mutation in rpsB, the gene encoding
 RT ribosomal protein S2";
 RT J. Bacteriol. 173:3291-3302(1991).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE OF 518-628 FROM N.A.
 RC STRAIN=JM101;
 RA Peng H., Hsieh M., Zao C., Chang H.-Y.;
 RT "Nucleotide sequence and expression in Escherichia coli of the
 RT Klebsiella pneumoniae dead gene";
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-20, AND CHARACTERIZATION.
 RX MEDLINE=96133880; PubMed=8552679;

RA Jones P.G., Milta M., Kim Y., Jiang W., Inouye M.;
 RT "Cold shock induces a major ribosomal-associated protein that unwinds
 RT double-stranded RNA in Escherichia coli";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:76-80(1996).
 CC -1- FUNCTION: HAS A HELIX-DESTABILIZING ACTIVITY. PLAYS A KEY ROLE IN
 CC OPTIMAL CELL GROWTH AT LOW TEMPERATURE AND IS REQUIRED FOR NORMAL
 CC CELL DIVISION. SUPPRESSOR OF A MUTANT DEFECTIVE IN RPSB GENE FOR
 CC RIBOSOMAL PROTEIN S2.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
 CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 535
 CC ONWARD AND IS SHORTER (553 AA) DUE TO A FRAMESHIFT.
 CC -----
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 CC EMBL: M63288; AAA23674.1; ALT_FRAME.
 CC EMBL: U18997; AAA57965.1; ALT_INIT.
 CC EMBL: AE000397; AAC76196.1; ALT_INIT.
 CC EMBL: U03750; AAA03626.1; -
 CC PIR: A42357; A42357.
 CC HSSP: 058083; 1HV8.
 CC Ecogen: EG10215; dead.
 CC InterPro: IPR001410; DEAD.
 CC InterPro: IPR000629; DEAD_box.
 CC InterPro: IPR001650; Helicase_C.
 CC Pfam: PF00270; DEAD.1.
 CC Pfam: PF00271; Helicase_C.1.
 CC SMART: SM00487; DEXDC.1.
 CC SMART: SM00490; HELICG.1.
 CC PROSITE: PS00039; DEAD_ATP_HELICASE.1.
 CC Hydroxylase; Helicase; ATP-binding; RNA-binding;
 KM Transcription regulation; Complete proteome.
 FT INIT_MET 0
 FT NP_BIND 49 56 ATP (BY SIMILARITY).
 FT SITE 155 158 DEAD BOX.
 FT DOMAIN 567 628 ARG/GLU/SIV-RICH.
 FT CONFLICT 443 443 G -> A (TN REF.2).
 SO SEQUENCE 628 AA; 70400 MW; 451528421DA26D99 CRC64;

 Query Match 58.3%; Score 35; DB 1; Length 628;
 Best Local Similarity 63.6%; Pred. No. 30;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 QY 1 AAEGLDTPRFS 11
 DB 304 AARGLDVERIS 314

 RESULT 10
 THIC_SALTI STANDARD; PRT; 631 AA.
 ID THIC_SALTI
 AC Q86326;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thiamine biosynthesis protein thic.
 GN THIC OR STY3721.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxId=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C718;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahinia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltham T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
 RA Krogan A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.,
 RT Complete genome sequence of a multiple drug resistant *Salmonella*
 RT *enterica* serovar Typhimurium.
 RL Nature 413:848-852(2001).
 CC -1- FUNCTION: Required for the synthesis of the hydromethylpyrimidine
 CC (HMP) moiety of thiamine (4-amino-2-methyl-5-
 CC hydroxymethylpyrimidine) (By similarity).
 CC -1- PATHWAY: Thiamine biosynthesis.
 CC -1- SIMILARITY: BELONGS TO THE THIC FAMILY.
 CC -----
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 CC -----
 CC EMBL: AL627279; CAD09480.1; -
 CC InterPro: IPR002817; Thic.
 CC Pfam: PF01964; Thic; 1.
 CC ProDom: PD007048; Thic; 1.
 CC TIGRFAMs: TIGR00190; thic; 1.
 CC Thiamine biosynthesis; Complete proteome.
 CC KW Thiamine biosynthesis; Complete proteome.
 CC SEQUENCE 631 AA; 70802 MW; A323C63038EFAAD CRC64;
 SO
 Query Match 58.3%; Score 35; DB 1; Length 631;
 Best Local Similarity 58.3%; Pred. No. 30;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AAEGLDTQRFSG 12
 Db 123 ADDGLDLRFTG 134
 RESULT 11
 THIC_SALTY STANDARD; PRT; 631 AA.
 ID THIC_SALTY STANDARD; PRT; 631 AA.
 AC Q9L917;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thiamine biosynthesis protein thic.
 GN THIC OR STM4164 OR STM41.33.
 OS *Salmonella typhimurium*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC *Salmonella*.
 CC NCBI_TaxID=602;
 ON [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGGC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Muiyaney E.,
 RA Ryan E., Sun H., Florita L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LT2.
 RL Nature 413:852-856(2001).
 CC -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF THE HYDROMETHYLPIRIMIDINE
 CC (HMP) MOIETY OF THIAMINE (4-AMINO-2-METHYL-5-
 CC HYDROXYMETHYLPIRIMIDINE) (BY SIMILARITY).
 CC -1- PATHWAY: Thiamine biosynthesis.
 CC -1- SIMILARITY: BELONGS TO THE THIC FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF170176; AF335523.1; -
 CC DR EMBL: AE008894; ALU22992.1; -
 CC DR StGene: SG27272; Thic.
 CC DR InterPro: IPR002817; Thic.
 CC Pfam: PF01964; Thic; 1.
 CC ProDom: PD007048; Thic; 1.
 CC TIGRFAMs: TIGR00190; thic; 1.
 CC Thiamine biosynthesis; Complete proteome.
 CC KW Thiamine biosynthesis; Complete proteome.
 CC SEQUENCE 631 AA; 70845 MW; 0A298124EC6644A CRC64;
 SO
 Query Match 58.3%; Score 35; DB 1; Length 631;
 Best Local Similarity 58.3%; Pred. No. 30;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AAEGLDTQRFSG 12
 Db 123 ADDGLDLRFTG 134
 RESULT 12
 DEAD_KLEPN STANDARD; PRT; 642 AA.
 ID DEAD_KLEPN STANDARD; PRT; 642 AA.
 AC P33906;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cold-shock DEAD-box protein A (ATP-dependent RNA helicase dead).
 GN DEAD OR CSDA.
 OS *Klebsiella pneumoniae*.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC *Klebsiella*.
 CC NCBI_TaxID=573;
 ON [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CG43;
 RX MEDLINE=9434279; PubMed=8056751;
 RA Peng H.L., Hsieh M.-J., Zao C.-L., Chang H.-Y.;
 RT "Nucleotide sequence and expression in *Escherichia coli* of the
 RT *Klebsiella pneumoniae* dead gene";
 RL J. Biochem. 115:409-414(1994).
 CC -1- FUNCTION: HAS A HELIX-DESTABILIZING ACTIVITY. PLAYS A KEY ROLE IN
 CC OPTIMAL CELL GROWTH AT LOW TEMPERATURE AND IS REQUIRED FOR NORMAL
 CC CELL DIVISION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: L08387; AAA61345.1; ALT_INT1.
 CC DR PIR: JX0314; JX0314.
 CC DR HSSP: Q58083; 1HW8.
 CC DR InterPro: IPR001410; DEAD.
 CC DR InterPro: IPR000629; DEAD-box.
 CC DR InterPro: IPR001650; Helicase_C.
 CC Pfam: PF00270; DEAD; 1.
 CC Pfam: PF00271; helicase_C; 1.
 CC SMART: SM00487; DEXDC; 1.
 CC SMART: SM00490; HELIC; 1.
 CC PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
 CC KW Hydrolyase; Helicase; ATP-binding; RNA-binding;

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RA RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Minari A., Mambut R., Wedler E., Wedler H., Weitzenecker T.,
RA Valters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -!- FUNCTION: ACTIVATOR OF THE GLUCUTROL DEHYDROGENASE GENE (GUTB).
CC -----
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CC -----
DR DR EMBL; L19113; AAA20676.1; -
DR EMBL; AB007637; BAA22759.1; -
DR EMBL; Z99107; CAB12453.1; -
DR Subtilist; BG10178; gutr.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 3.
KM Transcription regulation; DNA-binding; Activator; ATP-binding;
KM Complete proteome.
FT FT DNA_BIND 42 H-T-H MOTIF (BY SIMILARITY).
FT NP_BIND 200 ATP (POTENTIAL).
FT VARIANT 289 S -> R (IN GUTR). RESULTS IN THE
FT CONSTITUTIVE EXPRESSION OF GUTB).
SQ SEQUENCE 829 AA; 95076 MW; 2AF1B18F043BEFA51 CRC64;
OY 1 AAEGLDQRF 10
Db 459 AAAGLDARRF 468

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CC -1- SUBUNIT: HOMODIMER.
CC -1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPEPTIDE CHROMOPHORE.
CC -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC -----
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CC -----
CC EMBL: X61458; CAA43698.1; -.
CC PIR: S31280.
CC InterPro: IPR003594; ATPbind_ATPase.
CC InterPro: IPR003018; GAF.
CC InterPro: IPR004359; HIS_KIN_sig.
CC InterPro: IPR003661; His_kinA.
CC InterPro: IPR001610; PAC.
CC InterPro: IPR000700; PAS-assoc_C.
CC InterPro: IPR000014; PAS_domain.
CC InterPro: IPR001294; Phytochrome.
CC Pfam: PF00360; Phytochrome; 1.
CC Pfam: PF00512; signal; 1.
CC Pfam: PF00989; PAS; 2.
CC Pfam: PF01590; GAF; 1.
CC Pfam: PF02518; HATPase_C; 1.
CC PRINTS: PRO1033; PHYTOCHROME.
CC SMART: SM00065; GAF; 1.
CC SMART: SM00387; HATPase_C; 1.
CC SMART: SM00388; HisKA; 1.
CC SMART: SM00091; PAS; 2.
CC TIGRfam: TIGR00229; sensory_box; 2.
CC PROSITE: PS50109; HIS_KIN; 1.
CC PROSITE: PS50113; PAC; 1.
CC PROSITE: PS50112; PAS; 2.
CC PROSITE: PS50245; PHYTOCHROME_1; 1.
CC PROSITE: PS50246; PHYTOCHROME_2; 1.
CC Transcription regulation: Photoreceptor: Phytochrome; Chromophore;
CC Repeat; Multigene family.
CC KW DOMAIN 616 687 PAS 1.
CC FT DOMAIN 690 746 PAC.
CC FT DOMAIN 750 821 PAS 2.
CC FT DOMAIN 901 1121 HISTIDINE KINASE.
CC FT BINDING 324 324 CHROMOPHORE (BY SIMILARITY).
CC FT DOMAIN 352 358 POLY-GLY.
CC SEQENCE 1134 AA; 124706 MW; 42819B9FAAC398C CRC64;

Query Match 58.3%; Score 35; DB 1; Length 1134;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AEGLDTPQRF 10
   11:11111111
Db 827 AADGQDTEKF 836

RESULT 15
GLTB_AZOBR
ID GLTB_AZOBR STANDARD; PRT; 1515 AA.
AC 005755;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamate synthase [NADPH] large chain precursor (EC 1.4.1.13)
DE (Glutamate synthase alpha subunit) (NADPH-GOGAT) (GLTs alpha chain).
GN GLTB.
OS Azospirillum brasilense.
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;

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CC Azospirillum.
CC NCBI_Taxid=192;
CC [1]
CC SEQUENCE FROM N.A., AND SEQUENCE OF 37-56; 778-799 AND 1325-1345.
CC RP SPANNE-SE7 / ATCC 29145;
CC RC MEDLINE=93155143; Pubmed=8428988;
CC RX MEDLINE=93155143; Pubmed=8428988;
CC RA Pelanda R., Vancil M.A., Perego M., Plubelli L., Gallizzi A.,
CC Curti B., Zanetti G.;
CC RT "Glutamate synthase genes of the diazotroph Azospirillum brasilense.
CC Cloning, sequencing, and analysis of functional domains.";
CC J Biol. Chem. 268:3099-3106(1993).
CC [2]
CC SEQUENCE OF 834-927 FROM N.A.
CC RP STRAIN=RG;
CC RC MEDLINE=94075244; Pubmed=7902833;
CC RX Mandal A.K., Ghosh S.;
CC RA "Isolation of a glutamate synthase (GOGAT)-negative, photoautotrophically
CC N utilization-defective mutant of Azospirillum brasilense: cloning
CC and partial characterization of GOGAT structural gene.";
CC J. Bacteriol. 175:8024-8029(1993).
CC [3]
CC PARTIAL SEQUENCE.
CC RX MEDLINE=90335272; Pubmed=2198943;
CC RA Vancil M.A., Negri A., Zanetti G., Ronchi S., Curti B.;
CC RT "Structural studies on the subunits of glutamate synthase from
CC Azospirillum brasilense.";
CC RL Biochim. Biophys. Acta 1039:374-377(1990).
CC CC -1- CATALYTIC ACTIVITY. 2 L-glutamate + NADP(+) = L-glutamine + 2-
CC oxoglutarate + NADPH.
CC CC -1- COFACTOR: BINDS A 3FE-4S CLUSTER; FAD AND FMN.
CC CC -1- PATHWAY: NITROGEN METABOLISM, GLUTAMATE BIOSYNTHESIS.
CC CC THE CATALYZED REACTION BRINGS TOGETHER THE NITROGEN AND
CC CARBON METABOLISM.
CC CC -1- SUBUNIT: AGGREGATE OF 4 CATALYTICAL ACTIVE HETERODIMERS,
CC CONSISTING OF A LARGE AND A SMALL SUBUNIT.
CC CC -1- MISCELLANEOUS: GLUTAMINE BINDS TO THE LARGE SUBUNIT AND TRANSFERS
CC THE AMIDO GROUP TO 2-OXO-GLUTAMATE THAT APPARENTLY BINDS TO THE
CC SMALL SUBUNIT.
CC CC -1- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
CC -----
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CC -----
CC EMBL: AF192408; AAA22179.1; -.
CC DR EMBL: X71632; CAA50639.1; -.
CC DR PIR: B46602; B46602.
CC DR InterPro: IPR002489; DUF14.
CC DR InterPro: IPR003009; FMN_enzyme.
CC DR InterPro: IPR002932; Glu_synthase.
CC DR Pfam: PF01493; DUF14; 1.
CC DR Pfam: PF01645; Glu_synthase; 1.
CC KW Oxidoreductase; Iron-sulfur; 3Fe-4S; Flavoprotein; FAD; FMN; NADP;
CC Glutamate biosynthesis; Zymogen.
CC FT PROPEP 1 36
CC FT CHAIN 37 1515
CC FT NP_BIND 1085 1142 FMN (BY SIMILARITY).
CC FT METAL 1138 1138 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
CC FT METAL 1144 1144 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
CC FT METAL 1149 1149 IRON-SULFUR (3FE-4S) (BY SIMILARITY).
CC FT NP_BIND 1086 1142 FMN (BY SIMILARITY).
CC SEQENCE 1515 AA; 166018 MW; ED91321BDFCE92 CRC64;

Query Match 58.3%; Score 35; DB 1; Length 1515;
Best Local Similarity 70.0%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AEGLDTPQRF 11
   1111111111

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Tue Apr 15 10:21:36 2003

us-09-521-527c-1.open.rsp

Page 10

Db 683 AEGLOTHYFA 692

Search completed: April 15, 2003, 10:12:44
Job time : 13 secs

RESULT 2

Q960R6 PRELIMINARY; PRT; 235 AA.
 AC Q960R6; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 GN CD8A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21329138; PubMed=11435463;
 RA de La Calle-Martín O., Hernandez M., Ordí J., Casamitjana N.,
 RA Arostegui J.I., Caragol I., Ferrando M., Labrador M.,
 RA Rodriguez-Sanchez J.L., Espanol T.;
 RT "Familial CD8 deficiency due to a mutation in the CD8alpha gene."
 RL J. Clin. Invest. 108:117-117(2001).
 DR EMBL; AF039664; AAK72403.1; -.
 DR InterPro: IPR003006; 19_MHC.
 DR Pfam: PF00047; 19; 1.
 SQ SEQUENCE 235 AA; 25759 MW; FCCA347AAEF732BB CRC64;

Query Match 100.0%; Score 60; DB 4; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDTRFSG 12
 Db 80 AAEGLDTRFSG 91
 |||||

RESULT 3

Q87AW8 PRELIMINARY; PRT; 235 AA.
 AC Q87AW8; 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 GN CD8 antigen, alpha polypeptide (p32).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA Straussberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025715; AAH25715.1; -.
 SQ SEQUENCE 235 AA; 25669 MW; FCDPC9B5472D26BB CRC64;

Query Match 100.0%; Score 60; DB 4; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDTRFSG 12
 Db 80 AAEGLDTRFSG 91
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RESULT 4

Q9XSM6 PRELIMINARY; PRT; 235 AA.
 AC Q9XSM6; 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 GN alpha chain precursor.
 OS Saimiri sciureus (Common squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
 RN NCBI_TaxID=9521;
 RP SEQUENCE FROM N.A.
 RC STRAIN=92039;
 RA MEDLINE=992939362; PubMed=10369934;
 RA Ureta-Vidal A., Garcia Z., Lemmonier F.A., Kazanji M.;
 RT "Molecular characterization of CDNA encoding squirrel monkey (Saimiri
 sciureus) CD8 alpha and beta chains."
 RL Immunogenetics 49:718-721(1999).
 DR EMBL; AJ130818; CAB41462.1; -.
 DR HSSP; P01732; 1CD8
 DR InterPro: IPR003599; 19.
 DR InterPro: IPR003006; 19_MHC.
 DR InterPro: IPR002965; P-rich_extensn.
 DR Pfam: PF00047; 19; 1.
 DR PRINTS; PR01217; PRICHEXTENS.
 DR SMART; SM00409; IG; 1.
 KW signal.

Query Match 80.0%; Score 48; DB 6; Length 235;
 Best Local Similarity 81.8%; Pred. No. 0.28;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 AAEGLDTRFSG 12
 Db 81 ADGLDTRFSG 91
 |||||

RESULT 5

Q96D13 PRELIMINARY; PRT; 580 AA.
 AC Q96D13; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 GN Hypothetical 65.0 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA Straussberg R.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC001513; AAH01513.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 580 AA; 64958 MW; 9FB02B4160595E32 CRC64;

Query Match 65.0%; Score 39; DB 4; Length 580;
 Best Local Similarity 66.7%; Pred. No. 45;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAEGLDTRFSG 12
 Db 235 AAEGLDTRFSG 246
 |||||

RESULT 6

Q8TCG0 PRELIMINARY; PRT; 973 AA.
 AC Q8TCG0; 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 GN Hypothetical 110.2 kDa protein.
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RA Oltjenweider B., Obermaier B., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713725; CAD28515.1; -
KM Hypothetical protein.
SQ SEQUENCE 973 AA; 110185 MW; 0008E21D66E8CEFC CRC64;

Query Match
Best Local Similarity 65.0%; Score 39; DB 4; Length 973;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAEGLDTQRFSG 12
DB 235 AAECAEAGQFSG 246

RESULT 7
O9P253 PRELIMINARY; PRT; 986 AA.
AC O9P253; Q9H268;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE KIAA1475 protein (Vacuolar protein sorting protein 18)
DE (Fragment).
GN KIAA1475 OR VPS18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human
RT genes. XVII. The complete sequences of 100 new cDNA clones from brain
RT which code for large proteins in vitro.";
RL DNA Res. 7:143-150(2000).
RN [2]
RN SEQUENCE OF 14-986 FROM N.A.
RP MEDLINE=21147934; PubMed=11250079;
RA Huizing M., Didier A., Walenta J., Anikster V., Gahl W.A., Kramer H.;
RT "Molecular cloning and characterization of human VPS18, VPS11, VPS16,
RT and VPS33.";
RL Gene 264:241-247(2001).
DR EMBL; AB040908; BA9599.1; -
DR EMBL; AF308802; AAG34679.1; -
DR InterPro: IPR00547; Clathrin_repeat.
DR SMART: SM00299; CLH; 1.
FT NON_TER
FT SEQUENCE 986 AA; 111475 MW; 4BA494BE6ED58C94 CRC64;

Query Match
Best Local Similarity 65.0%; Score 39; DB 4; Length 986;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAEGLDTQRFSG 12
DB 248 AAECAEAGQFSG 259

RESULT 8
O8X6X9 PRELIMINARY; PRT; 631 AA.
AC O8X6X9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

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DE Thiamin biosynthesis, pyrimidine moiety (Thiamin biosynthesis protein
DE ThIC).
GN THIC OR Z5569 OR ECS4917.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Pfafel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lam A., Dimantanta E.T., Polunousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsuda E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005631; AAG59191.1; -
DR EMBL; AP002567; BAB38340.1; -
DR InterPro: IPR002817; ThIC.
DR Pfam: PF01964; ThIC; 1.
DR PRODOM: PD007048; ThIC; 1.
DR TIGRFAMs: TIGR00190; ThIC; 1.
KW Complete proteome.
SQ SEQUENCE 631 AA; 70814 MW; 5494CBBD9C036F2E CRC64;

Query Match
Best Local Similarity 63.3%; Score 38; DB 16; Length 631;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAEGLDTQRFSG 12
DB 123 ADDGDELRFSG 134

RESULT 9
Q8VUT2 PRELIMINARY; PRT; 817 AA.
ID Q8VUT2
AC Q8VUT2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Beta-1,3-xylanase.
DE AXNB.
OS Pseudomonas sp. ND137.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OX NCBI_TaxID=147640;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=ND137;
RA Aoki Y., Kitamura E., Myounga H., Kamel Y.;
RT "Protoplast production of red alga Porphyra yezoensis by recombinant
RT enzymes from Pseudomonas sp.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB063257; BAB79289.1; -
KM Xylan degradation; Hydrolase; Glycosidase.
SQ SEQUENCE 817 AA; 85650 MW; 6D453A7D6D202329 CRC64;

Query Match
Best Local Similarity 63.3%; Score 38; DB 2; Length 817;

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RT-PCR identification and characterization of a shrimp white spot syndrome virus (WSSV) gene that encodes a novel chimeric polypeptide of

RA de Souza A.P., Ten
RA Vallada H., Van SI
RA Zago M.A., Zatz M


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RT      "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL      Nature 406:151-159(2000).
DR      EMBL; AE004041; AAF85090.1; -.
KW      Complete proteome.
SQ      SEQUENCE 252 AA; 28014 MW; 4EB9FCBE739F01FB CRC64;

Query Match
Best Local Similarity 61.7%; Score 37; DB 16; Length 252;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 AAEGLDTPRF 10
        |||||
DB      240 AAEGLDTPRY 249

RESULT 13
Q9RBF7
ID      Q9RBF7      PRELIMINARY;      PRT;      299 AA.
AC      Q9RBF7;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      Formate dehydrogenase.
GN      FDSR.
OS      Alcaligenes eutrophus (Ralstonia eutropha).
OC      Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC      Ralstonia.
OX      NCBI_TaxID=510;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=H16;
RX      MEDLINE=20032351; PubMed=10564479;
RA      Oh J.I., Bowlen B.;
RT      "Dual control by regulatory gene fdsr of the fds operon encoding the
RT      NAD(+)-linked formate dehydrogenase of Ralstonia eutropha.";
RL      MOL Microbiol. 34:365-376(1999).
DR      EMBL; AA007718; CAB59983.1; -.
DR      InterPro: IPR003725; Mode.
DR      Pfam: PF02573; HTH_9; 1.
SQ      SEQUENCE 299 AA; 32319 MW; 43DD1AD3D40CA4BC CRC64;

Query Match
Best Local Similarity 61.7%; Score 37; DB 2; Length 299;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 AAEGLDTPRFSG 12
        |||||
DB      249 AAEGLDTPRREG 260

RESULT 14
O8XXX5
ID      O8XXX5      PRELIMINARY;      PRT;      363 AA.
AC      O8XXX5;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      Probable 3-isopropylmalate dehydrogenase oxidoreductase protein
DE      (EC 1.1.1.85).
GN      LEU1 OR RSC1988 OR RS03417.
OS      Ralstonia solanacearum (Pseudomonas solanacearum).
OC      Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC      Ralstonia.
OX      NCBI_TaxID=305;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=GM11000;
RX      MEDLINE=21681879; PubMed=11823852;
RA      Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA      Arlat M., Billault A., Brotlier P., Camus J.C., Catolico L.,
RA      Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA      Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA      Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,

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RA      Weissenbach J., Boucher C.A.;
RT      "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL      Nature 415:497-502(2002).
DR      EMBL; AL646067; CAD15690.1; -.
DR      InterPro: IPR001804; Isoch.
DR      InterPro: IPR004429; LeuB.
DR      Pfam: PF00180; Isoch; 1.
DR      TIGRfams; TIGR00169; LeuB; 1.
DR      PROSITE; PS00470; IDH_IMDH; 1.
KW      Oxidoreductase; Complete proteome.
SQ      SEQUENCE 363 AA; 39128 MW; 6343123C09817ACE CRC64;

Query Match
Best Local Similarity 61.7%; Score 37; DB 16; Length 363;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 AAEGLDTPRFS 11
        |||||
DB      161 AAEGLDTPRYS 171

RESULT 15
O9FKA8
ID      O9FKA8      PRELIMINARY;      PRT;      370 AA.
AC      O9FKA8;
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      Retroelement pol polyprotein-like.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=COLUMBIA;
RX      MEDLINE=98403884; PubMed=9734815;
RA      Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA      Tabata S.;
RT      "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT      Sequence features of the regions of 1,367,185 bp covered by 19
RT      physically assigned P1 and TAC clones.";
RL      DNA Res. 5:203-216(1998).
DR      EMBL; AB012243; BAB08885.1; -.
DR      InterPro: IPR005162; Retrotrans.-gag.
DR      InterPro: IPR001878; Znf_CCHC.
DR      Pfam: PF03732; Retrotrans.-gag; 1.
DR      Pfam: PF00098; Zf-CCHC; 1.
DR      SMART; SM00343; Znf_C2HC; 1.
KW      Polyprotein.
SQ      SEQUENCE 370 AA; 40618 MW; 3EBD9764902A6C17 CRC64;

Query Match
Best Local Similarity 61.7%; Score 37; DB 10; Length 370;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 GLDTPRFSG 12
        |||||
DB      201 GLDSARFSG 209

Search completed: April 15, 2003, 10:13:21
Job time : 32 secs

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GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 10:11:04 ; Search time 72 Seconds
(without alignments)
22.208 Million cell updates/sec

Title: us-09-521-527c-1
Perfect score: 60
Sequence: 1 AAEGIDTQRFSG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	12	21	AA824101
2	60	100.0	20	21	AA824103
3	60	100.0	114	17	AA98514
4	60	100.0	114	21	AA143644
5	60	100.0	121	20	AA143644
6	60	100.0	235	15	AA849550
7	60	100.0	235	20	AA849550
8	60	100.0	273	15	AA852862
9	60	100.0	376	21	AA52588
10	54	90.0	11	21	AA824102

11	40	66.7	8	17	AA898502	CD8 alpha chain re
12	40	66.7	8	21	AA143646	Fragment of a huma
13	40	66.7	10	17	AA898509	CD8 antigenist #4.
14	40	66.7	10	21	AA143649	Amino acid sequenc
15	39	65.0	80	22	AA423815	Human EST encoded
16	39	65.0	973	23	AB897191	Novel human protei
17	39	65.0	973	23	AB897191	Novel human protei
18	38	63.3	374	21	AA171530	Human intracellular
19	38	63.3	1204	22	AA85003	Corn POP2/CAPI tra
20	36	60.0	87	21	AA164916	Shrimp white spot
21	36	60.0	153	21	AA164914	Human 5' EST relat
22	36	60.0	373	21	AA164668	Arabidopsis thalia
23	36	60.0	420	21	AA164667	Arabidopsis thalia
24	36	60.0	461	21	AA164666	Arabidopsis thalia
25	36	60.0	553	18	AA35856	Human CD45 for use
26	35	58.3	278	21	AA32698	Eucalyptus grandis
27	35	58.3	504	23	AA017865	Pyrin domain conta
28	35	58.3	505	21	AA175701	Neisseria meningit
29	35	58.3	505	23	AA172960	Neisseria meningit
30	35	58.3	505	23	AA172969	Neisseria meningit
31	35	58.3	505	23	AA172982	Neisseria meningit
32	35	58.3	589	19	AA60667	E.coli cold shock
33	35	58.3	624	23	AA14675	Corynebacterium q1
34	35	58.3	646	22	AA134718	E. coli cellular p
35	35	58.3	646	22	AA138176	Salmonella typhi c
36	35	58.3	655	23	AB807264	Human ATRG polylep
37	35	58.3	732	22	AA81024	C glutamicum prote
38	35	58.3	736	22	AA862880	Membrane bound tra
39	35	58.3	736	23	AA178362	Cell differentiat
40	35	58.3	1006	22	AB824871	Novel human diagno
41	35	58.3	1038	22	AB824868	Novel human diagno
42	34	56.7	49	21	AA832691	Eucalyptus grandis
43	34	56.7	68	23	ABP08088	Human ORFX protein
44	34	56.7	105	21	AA171535	Wheat POP2/CAPI tr
45	34	56.7	301	22	AB81751	Novel human diagno

ALIGNMENTS

RESULT 1
ID AAB24101 standard; peptide: 12 AA.
XX AAB24101;
AC AAB24101;
XX AAB24101;
DT 23-JAN-2001 (first entry)
XX
XX Human CD8 antigenic peptide.
DE Human CD8 antigenic peptide.
XX
XX Human; CD8; antibody; antigenic; viral infection; tumour;
KW CD8+ cell; peripheral mononuclear blood cell.
XX
OS Homo sapiens.
XX
XX WO200055305-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05898.
XX
XX 12-MAR-1999; 99US-0124253.
XX
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX
XX Leturcc D;
XX
XX WPI; 2000-618917/59.
XX
XX Isolating CD8+ cells from peripheral mononuclear blood cells for use as
PT vehicles for combating viral infections and tumors, comprises using a
PT CD8 specific antibody that does not activate the cells -
XX

PS Claim 1; Page 15; 21pp; English.

XX CC The present invention describes a method for isolating CD8+ cells (I)

CC from peripheral mononuclear blood cells (PBMC) using an antibody which

CC specifically binds to the sequence AAEGLDTQRFSG (I) or a portion of (I)

CC on CD8 molecules present on the surface of CD8+ cells but does not

CC activate the CD8+ cells once bound. Also described are: (1) a hybridoma

CC cell line (II) which produces a monoclonal antibody that specifically

CC binds to CD8 molecules present on the surface of CD8+ cells but does not

CC activate the CD8+ cells; (2) a monoclonal antibody (III) produced by

CC (II); (3) a polypeptide comprising (I); useful for generating (III);

CC (4) a population of CD8+ cells isolated by (I); and (5) a kit, comprising

CC (III) and an agent which causes the dissociation of CD8+ cell-antibody

CC complex; (1) is useful for isolating human CD8+ cells from a sample of

CC isolated peripheral mononuclear blood cells. The isolated CD8+ cells have

CC importance as vehicles for combating viral infections and tumours.

XX CC

SQ Sequence 12 AA;

Query Match 100.0%; Score 60; DB 21; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.4e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAEGLDTQRFSG 12

Db 1 AAEGLDTQRFSG 12

RESULT 2

AA24103

ID AAB24103 standard; peptide: 20 AA.

XX AC AAB24103;

XX DT 23-JAN-2001 (first entry)

XX DE Human CD8 antigenic peptide #1.

XX KM Human CD8; antibody; antigenic; viral infection; tumour;

XX KW CD8+ cell; peripheral mononuclear blood cell.

XX OS Homo sapiens.

XX PN WO20005305-A1.

XX PD 21-SEP-2000.

XX PF 08-MAR-2000; 2000WO-US05898.

XX PR 12-MAR-1999; 99US-0124253.

XX PA (ORTH) ORTHO-MCNEIL PHARM INC.

XX PI Leturcq D;

XX DR WPI: 2000-618917/59.

XX PT Isolating CD8+ cells from peripheral mononuclear blood cells for use as

XX PT vehicles for combating viral infections and tumors, comprises using a

XX PT CD8 specific antibody that does not activate the cells

XX PS Disclosure: Page 8; 21pp; English.

XX CC The present invention describes a method for isolating CD8+ cells (I)

CC from peripheral mononuclear blood cells (PBMC) using an antibody which

CC specifically binds to the sequence AAEGLDTQRFSG (I) or a portion of (I)

CC on CD8 molecules present on the surface of CD8+ cells but does not

CC activate the CD8+ cells once bound. Also described are: (1) a hybridoma

CC cell line (II) which produces a monoclonal antibody that specifically

CC binds to CD8 molecules present on the surface of CD8+ cells but does not

CC activate the CD8+ cells; (2) a monoclonal antibody (III) produced by

CC (II); (3) a polypeptide comprising (I); useful for generating (III);

CC (4) a population of CD8+ cells isolated by (I); and (5) a kit, comprising

CC (III) and an agent which causes the dissociation of CD8+ cell-antibody

CC complex; (I) is useful for isolating human CD8+ cells from a sample of

CC isolated peripheral mononuclear blood cells. The isolated CD8+ cells have

CC importance as vehicles for combating viral infections and tumours. The

CC present sequence represents a human CD8 antigenic peptide, which is

CC given in the exemplification of the present invention.

XX CC

SQ Sequence 20 AA;

Query Match 100.0%; Score 60; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.5e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAEGLDTQRFSG 12

Db 5 AAEGLDTQRFSG 16

RESULT 3

AA98514

ID AAR98514 standard; peptide: 114 AA.

XX AC AAR98514;

XX DT 04-MAR-1997 (first entry)

XX DE CD8 alpha chain.

XX KM CD8 antagonist; inhibitor; T-cell activation; human; CD8 alpha chain;

XX KW thymic differentiation; transplantation; bone marrow; liver; heart; lung;

XX KW kidney; cornea; skin graft; graft versus host disease; therapy.

XX OS Homo sapiens.

XX PN MO9622106-A1.

XX PD 25-JUL-1996.

XX PF 17-JAN-1996; 96WO-US00310.

XX PR 17-JAN-1995; 95US-0372952.

XX PA (UYE-) UNIV JEFFERSON THOMAS.

XX PI Choksi S, Huang Z, Jameson BA, Kornigold R;

XX DR WPI: 1996-354307/35.

XX PT CD8 antagonist peptide(s) - used for inhibiting T cell activation,

XX PT partic. for treating transplant rejection or graft versus host

XX PT disease

XX PS Disclosure: Page 27-28; 44pp; English.

XX CC This sequence represents the human CD8 alpha chain. CD8 plays a major

CC role in the activation of mature T-cells, and in the thymic

CC differentiation process that leads to CD8 expression. CD8 is expressed

CC either as a homodimer (containing two alpha chains) or as a heterodimer

CC (an alpha and a beta chain). The CD8 CD82-like region is involved in

CC regulating T-cell activation. The antagonists of the invention contain

CC a fragment of this sequence (see AAR98501-R98505), and comprise a

CC molecular surface similar to at least a portion of human CD8 molecular

CC surface around the site of one of these peptides. The compounds of the

CC invention compete with CD8 so as to inhibit T-cell activation. They can

CC also be used to treat an individual who is about to undergo, is

CC undergoing, or has undergone a transplantation procedure such as bone

CC marrow, liver, heart, kidney, lung, islets, or cornea transplantation, or

CC skin grafts. The compounds can also be used to treat an individual

CC suspected of suffering from, or susceptible to graft versus host

CC disease.

XX CC

SQ Sequence 114 AA;

Query Match 100.0%; Score 60; DB 17; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDTQRFSG 12
| | | | | | | | | | | | | | | |
Db 59 AAEGLDTQRFSG 70

RESULT 4
AAV43644
ID AAV43644 standard; peptide; 114 AA.
XX
AC AAV43644;
XX
DT 11-FEB-2000 (first entry)
XX

DE Extracellular domain of the alpha chain of human CD8.

KM Extracellular domain; alpha chain; human CD8; T cell activation;
KW cytotoxic T lymphocyte activation; CTL activation;
KW graft versus host disease; CD8 antagonist; transplant;
KW allogeneic bone marrow transplant.

XX Homo sapiens.

OS Homo sapiens.

PN WO954345-A1.

XX 28-OCT-1999.

PF 21-APR-1999; 99WO-US08814.

XX 21-APR-1998; 98US-0082436.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Korgold R, Huang Z, Choksi S;

XX WPI; 2000-013224/01.

PT Novel CD8 antagonists used to inhibit cytotoxic T lymphocytes and

PS prevent immune responses -

XX Disclosure; Page 47-48; 67pp; English.

XX The present sequence represents the extracellular domain of the alpha

CC chain of human CD8. Regions of the alpha chain have been identified

CC which interact with other molecules in the mediation of immune responses

CC and activation of T cells. The specification describes peptides

CC that are CD8 antagonists, and that compete with these CD8 regions in

CC intermolecular interactions that involve CD8 which are associated with

CC cytotoxic T lymphocyte (CTL) activation. These peptides comprise a

CC molecular surface that corresponds to a molecular surface of human CD8

CC at amino acids 73-76, 38-46, 53-56, 60-67 or 53-67. The peptides can be

CC used in methods and compositions for therapeutically or prophylactically

CC treating graft versus host disease in patients who have or about to

CC undergo transplants, e.g. allogeneic bone marrow transplants. The

CC methods and compositions are also used to treat individuals who are

CC undergoing and/or who have undergone transplants, e.g. transplants of

CC heart, liver, lung, islets or cornea, and skin grafts. The methods are

CC also used to inhibit T cell activation in humans.

Query Match 100.0%; Score 60; DB 21; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDTQRFSG 12
| | | | | | | | | | | | | | | |
Db 60 AAEGLDTQRFSG 71

RESULT 5
AAI21689
ID AAI21689 standard; Protein; 121 AA.
XX
AC AAI21689;
XX
DT 18-AUG-1999 (first entry)
XX

DE Expressed fragment of human CD8 alpha protein.

KM T lymphocyte inhibition; CD8; immunosuppressive therapy; transplantation;
KW autoimmune disease; allergy; asthma; viral infection; cytotoxic;
KW corticosteroid; human; CD8 alpha protein.

XX Homo sapiens.

OS Homo sapiens.

PN WO921576-A1.

XX 06-MAY-1999.

XX 28-OCT-1998; 98WO-GB03235.

XX 28-OCT-1997; 97GB-0022779.

XX (ISIS-) ISIS INNOVATION LTD.

XX Gao GF, Gerth UC, Jakobsen BK, Sewell AK;

XX WPI; 1999-385058/32.

XX N-PSDB; AAX80968.

PT Inhibiting activity of T cells against target cells useful for

PS treating autoimmune diseases and allergy

XX Claim 9; Fig 1B; 79pp; English.

CC The invention describes a method for inhibiting activity of T lymphocytes

CC against a target cell by treating the cell with a soluble form of a CD8

CC molecule. The method is used as immunosuppressive therapy, e.g. in

CC patients undergoing transplantation, but also for treating autoimmune

CC diseases and allergy, e.g. exacerbation of asthma caused by viral

CC infection. The CD8 protein inhibits cytotoxic T cells in vitro or in

CC vivo, and its inhibitory activity can be adjusted by mutation. Treatment

CC with CD8 protein provides more selective immunosuppression than use of

CC corticosteroids. The present sequence represents the expressed fragment

CC of human CD8 alpha protein.

XX Sequence 121 AA;

XX Query Match 100.0%; Score 60; DB 20; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDTQRFSG 12
| | | | | | | | | | | | | | | |
Db 60 AAEGLDTQRFSG 71

RESULT 6
AAR9550
ID AAR9550 standard; Protein; 235 AA.

XX AAR9550;

XX 20-AUG-1994 (first entry)

XX Sequence of human CD8.

XX gp39; T-cell antigen; CD40 ligand; B-cell proliferation;
KW CD8; fusion protein; CD8; fusion protein.
XX Homo sapiens.

PN EP585943-A.
 XX
 PD 09-MAR-1994.
 XX
 PF 03-SEP-1993: 93EP-0114153.
 XX
 PR 04-SEP-1992: 92US-0940605.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Aruffo AA, Hollenbaugh D, Ledbetter JA, Aruffo A;
 XX WPI, 1994-076264/10.
 DR N-PSDB: AAQ57986.
 XX
 PT New nucleic acid encoding human gp39 T cell antigen - which is a
 PT ligand for the CD40 receptor, causing proliferation and
 PT differentiation of B cells and some cancer cells
 XX
 PS Disclosure: Fig 9; 39pp; English.
 XX
 CC The complete nucleic acid sequence of human gp39 (hgp39) protein
 CC (corresp. to cDNA) and the complete AA sequence of hgp39 are
 CC presented in AAQ57984 and AAR49548 respectively and contd. in plasmid
 CC CDM8-hgp39, deposited with the ATCC as E. coli, CDM8 MC1061/p3-hgp39
 CC and assigned accession No. 69050. The human T cell antigen gp39 is a
 CC ligand for the CD40 receptor. Soluble gp39 may be produced using the
 CC expression vector CD8-gp39. Chimeric genes may be constructed by
 CC fusing sequences encoding the extracellular domains of gp39 and
 CC CD8, pref. murine or human CD8 protein. Plasmid p3-shgp39 encoding
 CC the fusion protein of the extracellular domains from gp39 and CD8
 CC is deposited in E.coli as ATCC 69049.
 XX
 SO Sequence 235 AA:

Query Match 100.0%; Score 60; DB 15; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDTPRFSG 12
 |||||||||
 DB 80 AAEGLDTPRFSG 91

RESULT 7
 AAY21688
 ID AAY21688 standard; Protein; 235 AA.
 XX
 AC AAY21688;
 XX
 DT 18-AUG-1999 (first entry)
 XX
 DE Human CD8 alpha protein.
 XX
 KM T lymphocyte inhibition; CD8; immunosuppressive therapy; transplantation;
 KM autoimmune disease; allergy; asthma; viral infection; cytotoxic;
 KM corticosteroid; human; CD8 alpha protein.
 XX
 OS Homo sapiens.
 XX
 PN WO921576-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 28-OCT-1998: 98WO-GB03235.
 XX
 PR 28-OCT-1997: 97GB-0022779.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX
 PI Gao GF, Gerth UC, Jakobsen BK, Sewell AK;
 XX WPI: 1999-385058/32.
 DR

DR N-PSDB: AAX80967.
 XX
 XX Inhibiting activity of T cells against target cells useful for
 PT treating autoimmune diseases and allergy
 XX
 PS Disclosure: Fig 1A; 79pp; English.
 XX
 CC The invention describes a method for inhibiting activity of T lymphocytes
 CC against a target cell by treating the cell with a soluble form of a CD8
 CC molecule. The method is used as immunosuppressive therapy, e.g. in
 CC patients undergoing transplantation, but also for treating autoimmune
 CC diseases and allergy, e.g. exacerbation of asthma caused by viral
 CC infection. The CD8 protein inhibits cytotoxic T cells in vitro or in
 CC vivo, and its inhibitory activity can be adjusted by mutation. Treatment
 CC with CD8 protein provides more selective immunosuppression than use of
 CC corticosteroids. The present sequence represents a human CD8 alpha
 CC protein.
 XX
 SO Sequence 273 AA:

Query Match 100.0%; Score 60; DB 20; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDTPRFSG 12
 |||||||||
 DB 80 AAEGLDTPRFSG 91

RESULT 8
 AAR52862
 ID AAR52862 standard; Protein; 273 AA.
 XX
 AC AAR52862;
 XX
 DT 09-SEP-1994 (first entry)
 XX
 DE Human single chain CD8 in pPOW.
 XX
 KM CD8: single chain antibody; target binding polypeptide;
 KM antibody engineering; humanized antibody; pPOW; vector.
 XX
 OS Homo sapiens.
 XX
 PN WO9407921-A.
 XX
 PD 14-APR-1994.
 XX
 PF 24-SEP-1993: 93WO-AU00491.
 XX
 PR 25-SEP-1992: 92AU-0004973.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;
 PI Leah M, Malytil, Power BE;
 XX WPI: 1994-135515/16.
 DR N-PSDB: AAQ62954.
 XX
 PT New target-binding polypeptide(s) used for diagnosis, etc. -
 PT having a stable core polypeptide region with at least one
 PT target-binding region covalently attached, opt. mutated to alter
 PT specificity, etc.
 XX
 PS Disclosure: Page 38; 67pp; English.
 XX
 CC Human single-chain CD8 construct, designed for expression in a
 CC bacterial secretion vector such as pPOW, has the DNA sequence
 CC given in AAQ62954, encoding the protein given in AAR52862.
 XX
 SO Sequence 273 AA;

Query Match 100.0%; Score 60; DB 15; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGLDTRFSG 12
| | | | | | | | | | | | | |
DB 81 AAEGLDTRFSG 92

RESULT 9
AAV52588
ID AAV52588 standard; Protein; 376 AA.
XX
AC AAV52588;
XX
DT 28-FEB-2000 (first entry)
XX
DE Secreted modified Fas ligand, (secFL).
XX
KM Fas receptor; Fas ligand; FasL; apoptosis; screening; test compound;
interaction; affinity ligand; identification; purification; therapy;
overstimulation; premature cell death; fulminant liver damage;
understimulation; lymphoproliferative disorders; autoimmune disorder.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..211
FT /note= "Human CD8 secretory signal peptide"
FT 22..181
FT /note= "Human CD8 extracellular domain"
FT 184..189
FT /note= "Hexahistidine motif"
FT 192..197
FT /note= "Glu-Glu epitope tag"
FT 198..376
FT /note= "Human FasL extracellular domain"
XX
PN US6001962-A.
XX
PD 14-DEC-1999.
XX
PF 15-NOV-1996; 96US-0751512.
XX
PR 15-NOV-1996; 96US-0751512.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Ramer JK, Williams LT;
XX
DR WPI; 2000-061905/05.
XX
DR N-PSDB; AAZ46253.
XX
PT Modified Fas ligands for modeling and screening applications,
therapeutic applications and for use as affinity ligands -
XX
PS Claim 7; Fig 1; 20pp; English.
XX
CC This sequence represents a secreted modified human Fas ligand (secFL)
which comprises human CD8 secretory sequence and extracellular domain,
heterologous marker sequences (a hexahistidine motif, and a Glu-Glu
epitope tag) and the extracellular domain of Fas ligand (FasL). The
protein is useful for in vitro or in vivo modelling and screening of
test compounds to study the interaction between the Fas receptor and
the Fas ligand and the effects of that interaction on downstream events,
such as Fas mediated apoptosis. The protein may be used as an affinity
ligand for the identification and/or purification of the Fas receptors.
CC The protein is also useful for therapeutic applications in human and
non-human mammalian patients. Such disorders are characterised by
overstimulation, such as premature cell death and fulminant liver damage,
or understimulation of the Fas mediated pathway, such as
lymphoproliferative disorders and acceleration of autoimmune disorders.

XX Sequence 376 AA;
SQ

Query Match 100.0%; Score 60; DB 21; Length 376;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGLDTRFSG 12
| | | | | | | | | | | | | |
DB 80 AAEGLDTRFSG 91

RESULT 10
AAB24102
ID AAB24102 standard; peptide; 11 AA.
XX
AC AAB24102;
XX
DT 23-JAN-2001 (first entry)
XX
DE Human CD8 antigenic peptide CD8-3.
XX
KM Human; CD8; antibody; antigenic; viral infection; tumour;
CD8+ cell; peripheral mononuclear blood cell.
XX
OS Homo sapiens.
OS
PN MO200055305-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000MO-US05898.
XX
PR 12-MAR-1999; 99US-0124253.
XX
PA (ORTH) ORTHO-MCNEL PHARM INC.
XX
PI Leturcq D;
XX
DR WPI; 2000-618917/59.
XX
PT Isolating CD8+ cells from peripheral mononuclear blood cells for use as
vehicles for combating viral infections and tumors, comprises using a
CD8 specific antibody that does not activate the cells -
XX
PS Disclosure; Page 8; 21pp; English.
XX
CC The present invention describes a method for isolating CD8+ cells (1)
from peripheral mononuclear blood cells (PBMC) using an antibody which
specifically binds to the sequence AAEGLDTRFSG (1) or a portion of (1)
on CD8 molecules present on the surface of CD8+ cells but does not
activate the CD8+ cells once bound. Also described are: (1) a hybridoma
cell line (11) which produces a monoclonal antibody that specifically
binds to CD8 molecules present on the surface of CD8+ cells but does not
activate the CD8+ cells; (2) a monoclonal antibody (11) produced by
CC (11); (3) a polypeptide comprising (1); useful for generating (11);
CC (4) a population of CD8+ cells isolated by (1); and (5) a kit, comprising
CC (11) and an agent which causes the dissociation of CD8+ cell-antibody
complex. (1) is useful for isolating human CD8+ cells from a sample of
isolated peripheral mononuclear blood cells. The isolated CD8+ cells have
importance as vehicles for combating viral infections and tumors. The
present sequence represents a human CD8 antigenic peptide designated
CD8-3, which is given in the exemplification of the present invention.

SO Sequence 11 AA;

Query Match 90.0%; Score 54; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGLDTRFSG 11
| | | | | | | | | | | |
DB 1 AAEGLDTRFSG 11

PN WO9622106-A1.
 XX
 PD 25-JUL-1996.
 XX
 PF 17-JAN-1996; 96WO-US00310.
 XX
 PR 17-JAN-1995; 95US-0372952.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 PI Choksi S, Huang Z, Jameson BA, Kornigold R;
 XX WPI: 1996-354307/35.
 DR
 XX CD8 antagonist peptide(s) - used for inhibiting T cell activation,
 PT partic. for treating transplant rejection or graft versus host
 PT disease
 XX
 PS Claim 16; Page 29; 44pp: English.
 XX
 CC AAR8506-R98511 represent CD8 antagonists of the invention. CD8 plays a
 CC major role in the activation of mature T-cells, and in the thymic
 CC differentiation process that leads to CD8 expression. CD8 is expressed
 CC either as a homodimer (containing two alpha chains) or as a heterodimer
 CC (an alpha and a beta chain). The CD8 CDR2-like region is involved in
 CC regulating T-cell activation. The antagonists of the invention comprise
 CC a molecular surface similar to at least a portion of human CD8 molecular
 CC surface around the site of one of these peptides. The compounds of the
 CC invention compete with CD8 so as to inhibit T-cell activation. They can
 CC also be used to treat an individual who is about to undergo, is
 CC undergoing, or has undergone a transplantation procedure such as bone
 CC marrow, liver, heart, kidney, lung, islets, or cornea transplantation,
 CC or skin grafts. The compounds can also be used to treat an individual
 CC suspected of suffering from, or susceptible to graft versus host
 CC disease.
 CC
 XX
 XX Sequence 10 AA:
 SQ
 Query Match 66.7%; Score 40; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 AEGDGTQR 9
 |||||||
 DB 2 AEGDGTQR 9
 RESULT 14
 AAY43649
 ID AAY43649 standard; peptide: 10 AA.
 XX
 AC AAY43649;
 XX
 DT 11-FEB-2000 (first entry)
 XX
 DE Amino acid sequence of a human CD8 antagonist peptide.
 XX
 XX Extracellular domain: alpha chain; human CD8; T cell activation;
 KW cytotoxic T lymphocyte activation; CTL activation;
 KW graft versus host disease; CD8 antagonist; transplant;
 KW allogeneic bone marrow transplant; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 FH
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..10
 XX
 PN WO954345-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 21-APR-1999; 99WO-US08814.
 XX

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PX XX 21-APR-1998;          98US-0082436.
XX XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX XX
PI Korrngold R, Huang Z, Choksi S;
XX XX
DR WPI: 2000-013224/01.
XX XX
PT Novel CD8 antagonists used to inhibit cytotoxic T lymphocytes and
PR prevent immune responses -
XX XX
PS Disclosure: Page 49; 67pp; English.
XX XX
SS The present sequence represents a human CD8 antagonist peptide of the
CC invention. The specification describes peptides that are CD8 antagonists,
CC and that compete with regions within the extracellular domain of the
CC alpha chain of CD8 regions in intermolecular interactions that involve
CC CD8 which are associated with cytotoxic T lymphocyte (CTL) activation.
CC These peptides comprise a molecular surface that corresponds to a
CC molecular surface of human CD8 at amino acids 73-76, 38-46, 53-56,
CC 60-67 or 53-67. The peptides can be used in methods and compositions
CC for therapeutically or prophylactically treating graft versus host
CC disease in patients who have or about to undergo transplants, e.g.
CC allogeneic bone marrow transplants. The methods and compositions are
CC also used to treat individuals who are undergoing and/or who have
CC undergone transplants, e.g. transplants of heart, liver, lungs, islets
CC or cornea, and skin grafts. The methods are also used to inhibit T cell
CC activation in humans.
XX XX
SO Sequence 10 AA;

Query Match 66.7%; Score 40; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEGLDTOR 9
   |||||
DB 2 AEGLDTOR 9

RESULT 15
AAM23815
ID AAM23815 standard; Protein: 80 AA.
XX
AC AAM23815;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1340.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
EA (HYSE-) HKSEQ INC.
XX
X1 Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
X1 Cao Y, Dirmacac RA, Zhang J, Werhman T;
```

XX WPI: 2001-476164/51.
DR N-PSDB: AAH98474.
XX

XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX

XX Claim 20; Page 948; 1275pp; English.
XX

XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX

SQ Sequence 80 AA:

Query Match

Best Local Similarity 65.04; Score 39; DB 22; Length 80;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAEGLDTORFS 11

I I I I I I I I I I

DB 4 ACTGLINTORFS 14

Search completed: April 15, 2003, 10:12:26
Job time : 73 secs

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OM protein - protein search, using sw model

Run on: April 15, 2003, 10:13:29 ; Search time 38 Seconds
(without alignments)
19.306 Million cell updates/sec

Title: US-09-521-527c-1
Perfect score: 60
Sequence: 1 AABGLDTRFSG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep: *
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	35	58.3	646	10	US-09-815-242-10311
3	35	58.3	646	10	US-09-815-242-13769
4	35	58.3	655	9	US-10-066-521-13
5	35	58.3	732	9	US-09-738-626-4778
6	34	56.7	87	10	US-09-955-502-7
7	34	56.7	87	10	US-09-955-502-8
8	34	56.7	91	10	US-09-955-502-5
9	33	55.0	328	9	US-10-260-877-66
10	33	55.0	372	10	US-09-741-669-367
11	33	55.0	372	10	US-09-912-020-375
12	33	55.0	375	10	US-09-925-300-1674
13	33	55.0	550	10	US-09-895-828-452
14	33	55.0	635	10	US-09-815-242-13814
15	33	55.0	689	9	US-09-738-626-3675
16	33	55.0	2789	10	US-09-801-574-57
17	32	53.3	222	9	US-09-738-626-5078
18	32	53.3	241	9	US-10-102-806-610
19	32	53.3	260	9	US-09-738-626-4051

20	32	53.3	318	9	US-09-738-626-3557	Sequence 3557, Ap
21	32	53.3	467	9	US-09-738-626-6965	Sequence 6965, Ap
22	32	53.3	613	10	US-09-815-242-10990	Sequence 10990, A
23	32	53.3	806	9	US-09-815-242-11057	Sequence 11057, A
24	31.5	52.5	469	9	US-09-738-626-4947	Sequence 4947, Ap
25	31	51.7	22	10	US-09-896-888A-35	Sequence 35, Appl
26	31	51.7	23	10	US-09-896-888A-33	Sequence 33, Appl
27	31	51.7	27	10	US-09-896-888A-29	Sequence 29, Appl
28	31	51.7	28	10	US-09-896-888A-31	Sequence 31, Appl
29	31	51.7	43	10	US-09-896-888A-27	Sequence 27, Appl
30	31	51.7	87	10	US-09-955-502-6	Sequence 6, Appl1
31	31	51.7	88	10	US-09-955-502-9	Sequence 9, Appl1
32	31	51.7	90	10	US-09-955-502-10	Sequence 10, Appl1
33	31	51.7	116	9	US-09-738-626-6868	Sequence 6868, Ap
34	31	51.7	126	9	US-10-125-540-491	Sequence 491, Ap
35	31	51.7	126	10	US-09-764-870-491	Sequence 491, Ap
36	31	51.7	138	10	US-09-815-242-5416	Sequence 5416, Ap
37	31	51.7	142	10	US-09-815-242-12558	Sequence 12558, A
38	31	51.7	142	10	US-09-815-242-12561	Sequence 12561, A
39	31	51.7	204	9	US-09-738-626-4120	Sequence 4120, Ap
40	31	51.7	333	9	US-10-101-464A-561	Sequence 561, App
41	31	51.7	338	10	US-09-815-242-5727	Sequence 5727, Ap
42	31	51.7	341	10	US-09-820-044-2	Sequence 2, Appl1
43	31	51.7	341	10	US-09-815-242-12158	Sequence 12158, A
44	31	51.7	369	10	US-09-925-300-1070	Sequence 1070, Ap
45	31	51.7	370	10	US-09-862-027-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-963-790A-2
; Sequence 2, Application US/09963790A
; Patient No. US20020115161A1
; GENERAL INFORMATION:
; APPLICANT: FARMICK, Mike, et al.
; FILE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE DEAD GENE
; TITLE REFERENCE: 032301 WD 230
; CURRENT APPLICATION NUMBER: US/09/963, 790A
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-963-790A-2

Query Match 58.3% Score 35; DB 10; Length 624;
Best Local Similarity 63.6% Pred. No. 65;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AABGLDTRFSG 11
DB 293 AARGIDVERIS 303

RESULT 2
US-09-815-242-10311
; Sequence 10311, Application US/09815242
; Patient No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Traxick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10311
LENGTH: 646
TYPE: PRT
ORGANISM: Escherichia coli
US-09-815-242-10311

Query Match 58.3%; Score 35; DB 10; Length 646;
Best Local Similarity 63.6%; Pred. No. 68;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAEGLDQRF 11
DB 322 AARGLDVERIS 332

RESULT 3
US-09-815-242-13769

Sequence 13769, Application US/09815242
Patent No. US20020061369A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13769
LENGTH: 646
TYPE: PRT
ORGANISM: Salmonella typhi
US-09-815-242-13769

Query Match 58.3%; Score 35; DB 10; Length 646;
Best Local Similarity 63.6%; Pred. No. 68;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAEGLDQRF 11
DB 322 AARGLDVERIS 332

RESULT 4
US-10-066-521-13

Sequence 13, Application US/10066521
Publication No. US20030027757A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
APPLICANT: Wang, Weiye
APPLICANT: Blatcher, Maria
TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
FILE REFERENCE: 07334-334001
CURRENT APPLICATION NUMBER: US/10/066,521
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/318,645
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/265,231
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 655
TYPE: PRT
ORGANISM: Homo sapiens
US-10-066-521-13

Query Match 58.3%; Score 35; DB 9; Length 655;
Best Local Similarity 70.0%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAEGLDQRF 10
DB 417 AAEGLDQRF 426

RESULT 5
US-09-738-626-4778

Sequence 4778, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/37484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4778
LENGTH: 732

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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4778
Query Match
Best Local Similarity 58.3%; Score 35; DB 9; Length 732;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AEGIDTQRFSG 11
   ||||| : |
DB 401 AARGDVERIS 411

RESULT 6
US-09-955-502-7
; Sequence 7, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-955-502-7
Query Match
Best Local Similarity 56.7%; Score 34; DB 10; Length 87;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AEGIDTQRFSG 12
   ||||| : |
DB 14 AEGIDFQLYPG 24

RESULT 7
US-09-955-502-8
; Sequence 8, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Haemophilus ducreyi
US-09-955-502-8
Query Match
Best Local Similarity 56.7%; Score 34; DB 10; Length 87;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AEGIDTQRFSG 12
   ||||| : |
DB 14 AEGIDFQLYPG 24
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RESULT 8
US-09-955-502-5
; Sequence 5, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Actinobacillus actinomycetemcomitans
US-09-955-502-5
Query Match
Best Local Similarity 56.7%; Score 34; DB 10; Length 91;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AEGIDTQRFSG 12
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DB 14 AEGIDFQLYPG 24

RESULT 9
US-10-260-877-66
; Sequence 66, Application US/10260877
; Publication No. US20030021813A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Chovan, Linda E.
; APPLICANT: Hessler, Paul E.
; APPLICANT: Reich, Karl A.
; TITLE OF INVENTION: ESSENTIAL BACTERIA GENES AND GENOME
; TITLE OF INVENTION: SCANNING IN HAEMOPHILUS INFLUENZAE FOR THE IDENTIFICATION OF
; FILE REFERENCE: 6565.US.PI
; CURRENT APPLICATION NUMBER: US/10/260,877
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/649,145
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 328
; TYPE: PRT
; ORGANISM: H. influenzae
US-10-260-877-66
Query Match
Best Local Similarity 55.0%; Score 33; DB 9; Length 328;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEGIDTOR 9
   ||||| : |
DB 286 AAGSDAQR 294

RESULT 10
US-09-741-669-367
; Sequence 367, Application US/09741669
; Patent No. US20020022718A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
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RESULT 12
US-09-925-300-1674
Sequence 1674, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben,
TIME OF INVENTION: Nucleic Acids, proteins and Antibodies

RESULT 14
US-09-815-242-13814
; Sequence 13814, Application US/09815242

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; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13814
; TYPE: PRF
; LENGTH: 635
; ORGANISM: Salmonella typhi
; US-09-815-242-13814

Query Match          55.0%; Score 33; DB 10; Length 635;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 DMOREFSG 12
DB 427 ETOREFSG 433

RESULT 15
US-09-738-626-3675
; Sequence 3675; Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: YATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
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; SEQ ID NO 3675
; LENGTH: 689
; TYPE: PRF
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-3675

Query Match          55.0%; Score 33; DB 9; Length 689;
Best Local Similarity 58.3%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAEGLDIOREFSG 12
DB 608 AEEGLAEQEFNG 619
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Search completed: April 15, 2003, 10:19:25
Job time : 40 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 10:11:09 ; Search time 29 Seconds
(without alignments)
12.175 Million cell updates/sec

Title: US-09-521-527c-1

Perfect score: 60

Sequence: 1 AAEGDPTGRFSG 12

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	60	100.0	114	5	PCR-US96-00310-1
5	60	100.0	235	1	US-07-940-605A-12
6	60	100.0	235	2	US-08-690-096-12
7	60	100.0	273	2	US-08-403-853-12
8	60	100.0	376	3	US-08-751-512-8
9	44	73.3	15	4	US-08-875-309-15
10	44	73.3	16	4	US-08-875-309-16
11	40	66.7	8	1	US-08-372-952-3
12	40	66.7	8	4	US-08-875-309-3
13	40	66.7	8	5	PCR-US96-00310-3
14	40	66.7	10	1	US-08-372-952-6
15	40	66.7	10	4	US-08-875-309-6
16	40	66.7	10	5	PCR-US96-00310-6
17	36	60.0	553	3	US-08-630-172-13
18	36	60.0	553	4	US-09-375-419-13
19	35	58.3	78	2	US-08-245-511-39
20	35	58.3	78	2	US-08-600-993A-39
21	34	56.7	751	4	US-09-036-987A-24
22	34	56.7	751	4	US-09-370-700-24
23	32	53.3	513	2	US-09-122-230-7
24	31.5	52.5	107	2	US-08-888-366-14
25	31.5	52.5	107	2	US-08-888-366-20
26	31.5	52.5	107	2	US-08-888-366-26
27	31.5	52.5	107	3	US-08-397-411-2

28	31	51.7	79	2	US-08-469-537A-49	Sequence 49, Appl
29	31	51.7	148	4	US-09-134-001C-3640	Sequence 3640, Ap
30	31	51.7	256	2	US-08-469-537A-58	Sequence 58, Appl
31	31	51.7	266	2	US-07-857-224B-75	Sequence 75, Appl
32	31	51.7	282	2	US-08-701-191A-19	Sequence 19, Appl
33	31	51.7	287	1	US-07-952-817-24	Sequence 24, Appl
34	31	51.7	341	4	US-09-149-624-2	Sequence 2, Appl1
35	31	51.7	425	4	US-08-462-467B-16	Sequence 16, Appl
36	31	51.7	432	3	US-08-985-908-31	Sequence 31, Appl
37	31	51.7	476	4	US-09-306-593-9	Sequence 9, Appl1
38	31	51.7	649	4	US-08-462-467B-20	Sequence 20, Appl
39	31	51.7	717	6	5262177-5	Patent No. 5262177
40	31	51.7	719	2	US-08-520-933-3	Sequence 3, Appl1
41	31	51.7	719	4	US-09-285-040-3	Sequence 31, Appl
42	31	51.7	738	6	5262177-2	Patent No. 5262177
43	31	51.7	1495	4	US-08-462-467B-12	Sequence 12, Appl
44	31	51.7	3218	1	US-08-764-100-27	Sequence 27, Appl
45	30	50.0	14	4	US-09-242-435-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-466-368-8
Sequence 8, Application US/08466368
Patent No. 6093539
GENERAL INFORMATION:
APPLICANT: Maddon, Paul J.
APPLICANT: Littman, Dan R.
APPLICANT: Chess, Leonard
APPLICANT: Axel, Richard
APPLICANT: Weiss, Robin
APPLICANT: McDougall, J. S.
TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN
TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,368
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 24577-EL-B/JFW/KKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Active-site
LOCATION: 1..102
US-08-466-368-8

Query Match 100.0%; Score 60; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDTORFSG 12
DB 59 AAEGLDTORFSG 70

RESULT 2

US-08-372-952-1
Sequence 1, Application US/08372952
Patent No. 5645837
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korngold, Robert
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5645837ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,952
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-372-952-1

Query Match 100.0%; Score 60; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDTORFSG 12
DB 59 AAEGLDTORFSG 70

RESULT 3

US-08-875-309-1
Sequence 1, Application US/08875309
Patent No. 6180600
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korngold, Robert

APPLICANT: Huang, Ziwel
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180600ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,309
FILING DATE: 26-NOV-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE: 17-JAN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-309-1

Query Match 100.0%; Score 60; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGLDTORFSG 12
DB 59 AAEGLDTORFSG 70

RESULT 4

PCT-US96-00310-1
Sequence 1, Application PC/TUS9600310
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korngold, Robert
APPLICANT: Huang, Ziwel
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1752
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-00310-1

Query Match 100.0%; Score 60; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGLDTORFSG 12
DB 59 AAEGLDTORFSG 70

RESULT 5
US-07-940-605A-12
Sequence 12, Application US/07940605A
Patent No. 5540926
GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,605A
FILING DATE: 04-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-940-605A-12

Query Match 100.0%; Score 60; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGLDTORFSG 12
DB 80 AAEGLDTORFSG 91

RESULT 6
US-08-690-096-12
Sequence 12, Application US/08690096
Patent No. 5945513
GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,096
FILING DATE: 31-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,605
FILING DATE: 04-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-690-096-12

Query Match 100.0%; Score 60; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGLDTORFSG 12
DB 80 AAEGLDTORFSG 91

RESULT 7
US-08-403-853-12
Sequence 12, Application US/08403853
Patent No. 5844094
GENERAL INFORMATION:
APPLICANT: HUDSON, Peter J.
APPLICANT: LAH, Maria
APPLICANT: KORFF, Alex A.
APPLICANT: IRVING, Robert A.

APPLICANT: ATWELL, John L.
APPLICANT: MALBY, Robyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BERT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-853-12

Query Match 100.0%; Score 60; DB 2; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGLDTRFSG 12
DB 81 AAEGLDTRFSG 92

RESULT 8
US-08-751-512-8
Sequence 8, Application US/08751512
Patent No. 6001962
GENERAL INFORMATION:
APPLICANT: Ramer, J. Kevin
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: Modified FAS Ligands
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREM LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,512
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Matthew B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 02307K-07100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-751-512-8

Query Match 100.0%; Score 60; DB 3; Length 376;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGLDTRFSG 12
DB 80 AAEGLDTRFSG 91

RESULT 9
US-08-875-309-15
Sequence 15, Application US/08875309
Patent No. 6180600
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Krongold, Robert
APPLICANT: Huang, Zilwei
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz MacKiewicz & No. 6180600r1s
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,309
FILING DATE: 26-NOV-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE: 17-JAN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-309-15

Query Match 73.3%; Score 44; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAEGLDTR 9
|||||||
Db 7 AAEGLDTR 15

RESULT 10

US-08-875-309-16
Sequence 16, Application US/08875309
Patent No. 6180600
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korngold, Robert
APPLICANT: Huang, Ziwei
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180600r1s
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,309
FILING DATE: 26-NOV-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE: 17-JAN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-309-16

Query Match 73.3%; Score 44; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAEGLDTR 9
|||||||
Db 8 AAEGLDTR 16

RESULT 11

US-08-372-952-3
Sequence 3, Application US/08372952
Patent No. 5645837
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korngold, Robert
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5645837r1s
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,952
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-372-952-3

Query Match 66.7%; Score 40; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AEGIDTR 9
|||||||
Db 1 AEGIDTR 8

RESULT 12

US-08-875-309-3
Sequence 3, Application US/08875309
Patent No. 6180600
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korngold, Robert
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180600r1s
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA

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?
?      ZIP: 19103
?      COMPUTER READABLE FORM:
?      MEDIUM TYPE: Floppy disk
?      COMPUTER: IBM PC compatible
?      OPERATING SYSTEM: PC-DOS/MS-DOS
?      SOFTWARE: Wordperfect
?      CURRENT APPLICATION DATA:
?      APPLICATION NUMBER: US/08/875,309
?      FILING DATE: 26-NOV-1997
?      CLASSIFICATION: 424
?      PRIOR APPLICATION DATA:
?      APPLICATION NUMBER: PCT/US96/00310
?      FILING DATE: 17-JAN-1996
?      CLASSIFICATION: 424
?      PRIOR APPLICATION DATA:
?      APPLICATION NUMBER: US 08/372,952
?      FILING DATE: 17-JAN-1995
?      CLASSIFICATION: 424
?      ATTORNEY/AGENT INFORMATION:
?      NAME: Deluca, Mark
?      REGISTRATION NUMBER: 33,229
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: 215-568-3100
?      TELEFAX: 215-568-3439
?      INFORMATION FOR SEQ ID NO: 3:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 8 amino acids
?      TYPE: amino acid
?      TOPOLOGY: linear
?      MOLECULE TYPE: protein
?
US-08-875-309-3

Query Match
Best Local Similarity 66.7%; Score 40; DB 4; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AEGIDTOR 9
        11111111
Db      1 AEGIDTOR 8

RESULT 13
PCT-US96-00310-3
; Sequence 3, Application PC/TUS9600310
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Choksi, Swati
; APPLICANT: Korgold, Robert
; APPLICANT: Huang, Ziwel
; TITLE OF INVENTION: CD8 Antagonists
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00310
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/372,952
; FILING DATE: 17-JAN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

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?
?      NAME: Deluca, Mark
?      REGISTRATION NUMBER: 33,229
?      REFERENCE/DOCKET NUMBER: TJU-1752
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: 215-568-3100
?      TELEFAX: 215-568-3439
?      INFORMATION FOR SEQ ID NO: 3:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 8 amino acids
?      TYPE: amino acid
?      TOPOLOGY: linear
?      MOLECULE TYPE: protein
?
PCT-US96-00310-3
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Query Match
Best Local Similarity 66.7%; Score 40; DB 5; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AEGIDTOR 9
        11111111
Db      1 AEGIDTOR 8
```

```

RESULT 14
US-08-372-952-6
; Sequence 6, Application US/08372952
; Patent No. 5645837
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Choksi, Swati
; APPLICANT: Korgold, Robert
; TITLE OF INVENTION: CD8 Antagonists
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,952
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1440
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
?
US-08-372-952-6

Query Match
Best Local Similarity 66.7%; Score 40; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2 AEGLDTOR 9
|||||||
Db 2 AEGLDTOR 9

RESULT 15
US-08-875-309-6

; Sequence 6, Application US/08875309
; Patent No. 6180600
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Choksi, Swati
; APPLICANT: Korngold, Robert
; APPLICANT: Huang, Ziwei
; TITLE OF INVENTION: CD8 Antagonists
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 61806000ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,309
; FILING DATE: 26-NOV-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00310
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/372,952
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1772
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ. ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 10 amino acids
; TOPOLOGY: circular
; MOLECULE TYPE: protein
; US-08-875-309-6

Query Match 66.7%; Score 40; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEGLDTOR 9
|||||||
Db 2 AEGLDTOR 9

Search completed: April 15, 2003, 10:13:56
Job time : 31 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 10:18:44 ; Search time 14 Seconds

(without alignments)
82.401 Million cell updates/sec

Title: US-09-521-527C-1

Perfect score: 60

Sequence: 1 AAEGLDPTORFSG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 1580

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR73:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	28	46.7	11	2 A35594	buccalin - Callifor
2	23	38.3	9	2 F41978	callifmrfamide 6 -
3	22	36.7	9	2 E41978	callifmrfamide 5 -
4	22	36.7	9	2 G41978	callifmrfamide 7 -
5	22	36.7	12	2 G49410	t-complex polypept
6	22	36.7	12	2 A33099	163k exoantigen -
7	21	35.0	10	2 PNO136	pepsin (EC 3.4.23.
8	21	35.0	12	2 PH1481	T-cell receptor be
9	20	33.3	12	2 S07436	tachykinin - Afric
10	19	31.7	8	2 S13661	polygalacturonase
11	19	31.7	9	2 B33098	231k exoantigen -
12	18	30.0	9	2 D57444	neuropeptide Grb-A
13	18	30.0	10	2 PT0251	Ig heavy chain CRD
14	18	30.0	12	2 PH0920	T-cell receptor be
15	17	28.3	7	2 PT0529	T-cell receptor be
16	17	28.3	10	2 S70721	heat shock protein
17	17	28.3	11	2 S07201	physalaemin - frog
18	17	28.3	11	2 S19775	wound-induced prot
19	16	26.7	7	2 S09066	globulin IV alpha
20	16	26.7	8	2 B24749	neuropeptide B - b
21	16	26.7	8	2 S71919	alcohol dehydrogen
22	16	26.7	9	2 A61230	caesquestrin, car
23	16	26.7	9	2 C24180	fibrinogen beta ch
24	16	26.7	10	2 S33844	alpha-2-macroglobu
25	16	26.7	10	2 PH0946	T-cell receptor be
26	16	26.7	11	1 SPHO	substance P - hors
27	16	26.7	11	1 A60654	substance P - quin
28	16	26.7	11	1 JN0023	substance P - chic
29	16	26.7	11	2 S23306	substance P - Atla

30	16	26.7	11	2 A61512	variant surface gl
31	16	26.7	11	2 PT0287	Ig heavy chain CRD
32	16	26.7	11	2 PT0217	T-cell receptor be
33	16	26.7	11	2 A48973	glucosylase A1 (E
34	16	26.7	11	2 H84082	hypothetical prote
35	16	26.7	12	2 S01749	collagen alpha 1(I
36	16	26.7	12	2 S25039	Ig heavy chain V r
37	16	26.7	12	2 PH0802	T-cell receptor al
38	16	26.7	12	2 B32521	hexokinase (EC 2.7
39	16	26.7	12	2 B32521	aminotransferase c
40	16	26.7	12	4 PC2123	T-cell receptor be
41	15	25.0	6	2 PT0718	T-cell receptor be
42	15	25.0	7	2 PT0663	callifmrfamide 8 -
43	15	25.0	8	2 H41978	T-cell receptor be
44	15	25.0	8	2 PT0554	phyllocerulolein -
45	15	25.0	9	2 A61357	

ALIGNMENTS

RESULT 1
A35594
buccalin - California sea hare
C:Species: Aplysia californica (California sea hare)
C:Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 24-Jun-1993
C:Accession: A35594
R:Cropper, E.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K
Proc. Natl. Acad. Sci. U.S.A. 85, 6177-6181, 1988
A:Title: Structure and action of buccalin: a modulatory neuropeptide localized to an
A:Reference number: A35594; MUID:88320404; PMID:3413086
A:Accession: A35594
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <CRO>

Query Match 46.7%; Score 28; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. 48;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 GLDPTORFSG 12
DB 1 GMDSLAFSG 9

RESULT 2
F41978
callifmrfamide 6 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: F41978
R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Tho
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (d
A:Reference number: A41978; MUID:92196111; PMID:1549595
A:Accession: F41978
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DUV>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 38.3%; Score 23; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 AAEGLDPTORF 10
DB 1 ASGQDFMRF 9

RESULT 3
E41978

callIFMRamide 5 - bluebottle fly (Calliphora vomitoria)

C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999

C:Accession: E41978

R:Duve, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; MUID:92196111; PMID:1549595

A:Accession: E41978

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <DUV>

C:Keywords: amidated carboxyl end; neuropeptide

F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match

Best Local Similarity 36.7%; Score 22; DB 2; Length 9;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 AEGDTRRF 10

DB 1 AFGDFMRF 9

RESULT 4

callIFMRamide 7 - bluebottle fly (Calliphora vomitoria)

C:Species: Calliphora vomitoria

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999

C:Accession: G41978

R:Duve, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; MUID:92196111; PMID:1549595

A:Accession: G41978

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <DUV>

C:Keywords: amidated carboxyl end; neuropeptide

F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match

Best Local Similarity 36.7%; Score 22; DB 2; Length 9;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 AEGDTRRF 10

DB 1 AFGDFMRF 9

RESULT 5

t-complex polypeptide 1 homolog (peak 6b fraction) - rabbit (fragment)

N:Alternate names: Chaperonin homolog (peak 6b)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 04-Sep-1998

C:Accession: G49410

R:Rommelaere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.; An
Proc. Natl. Acad. Sci. U.S.A. 90, 11975-11979, 1993

A:Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven rela

A:Reference number: A49410; MUID:94089752; PMID:7903455

A:Accession: G49410

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <ROM>

C:Keywords: reticulocyte

C:Superfamily: molecular chaperone t-complex-type

Query Match

Best Local Similarity 36.7%; Score 22; DB 2; Length 12;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 AEGDTRRF 9

DB 1 AFGDFMRF 9

DB 4 ANTCMDTRK 12

RESULT 6

A:33099

163k exantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C:Accession: A33099

R:Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: A33099

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <NIC>

Query Match

Best Local Similarity 36.7%; Score 22; DB 2; Length 12;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 GDTQREFSG 12

DB 1 GVTQREFVG 9

RESULT 7

pepsin (EC 3.4.23.-) 4 - horse (fragment)

N:Alternate names: pepsin (PI 2.6)

C:Species: Equus caballus (domestic horse)

C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1999

C:Accession: PNO136

R:Gonchar, M.V.; Lavrenova, G.I.; Rudenskaya, G.N.; Galda, A.V.; Stepanov, V.M.

Biohimia 49, 1026-1037, 1984

A:Title: Multiple forms of horse pepsin.

A:Reference number: PNO133; MUID:84281135; PMID:6432065

A:Accession: PNO136

A:Molecule type: protein

A:Residues: 1-10 <GON>

A:Note: article in Russian with English abstract

C:Superfamily: aspartic proteinase; hydrolase; protein digestion

Query Match

Best Local Similarity 35.0%; Score 21; DB 2; Length 10;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 AEGDTRF 6

DB 2 ATREGLE 7

RESULT 8

T-cell receptor beta chain (clone A24/PEG2) - mouse (fragment)

P:1481

C:Species: Mus musculus (house mouse)

C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995

C:Accession: PH1481

R:Casanova, J.L.; Martinou, F.; Gounluer, H.; Barra, C.; Pannetier, C.; Regnault, A.;

J. Exp. Med. 177, 811-820, 1993

A:Title: T cell receptor selection by and recognition of two class I major histocompa

A:Reference number: PH1430; MUID:93171821; PMID:8436911

A:Accession: PH1481

A:Molecule type: mRNA

A:Residues: 1-12 <CAS>

A:Experimental source: cytoytic T-lymphocyte

A:Note: the authors translated the codon GGT for residue 2 as Ala and GCT for residue

C:Superfamily: immunoglobulin homology

C:Keywords: receptor; T-cell

Query Match 35.0%; Score 21; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Qy 1 AAGLDTORFSG 12
||| :||
Db 3 AAGC--AEQFPG 12

RESULT 9

S07436
tachykinin - African tree frog (*Kassina maculata*)

N:Alternate names: hylambatin

C:Species: *Kassina maculata*

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000

C:Accession: S07436

R:Yasuhara, T.; Erspamer, G.F.; Erspamer, V.

Biomed. Res. 2, 613-617, 1981

A:Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in t

A:Reference number: S07436

A:Accession: S07436

A:Molecule type: protein

A:Residues: 1-12 <YAS>

A:Experimental source: skin

A>Note: the source is designated as Hylambates maculatus

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 33.3%; Score 20; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 DNGRFSG 12
||| :||
Db 4 DPDFRYG 10

RESULT 10

S13661

polygalacturonase (EC 3.2.1.15) isoform PG2 - fungus (*Sclerotinia sclerotiorum*) (fragment

N:Alternate names: endopolygalacturonase; pectin depolymerase; pectinase

C:Species: *Sclerotinia sclerotiorum*

C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998

C:Accession: S13661

R:Waksman, G.; Keon, J.P.R.; Turner, G.

Biochim. Biophys. Acta 1073, 43-48, 1991

A:Title: Purification and characterization of two endopolygalacturonases from *Sclerotinia*

A:Reference number: S13661; PMID:91120822; PMID:1991145

A:Accession: S13661

A:Molecule type: protein

A:Residues: 1-8 <MAK>

C:Function:

A:Description: involved in pectin degradation

C:Keywords: glycosidase; hydrolase

Query Match 31.7%; Score 19; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TORFSG 12
||| :||
Db 3 TDTFSG 8

RESULT 11

B33098

23k exoantigen - malaria parasite (*Plasmodium falciparum*) (fragments)

C:Species: *Plasmodium falciparum*

C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C:Accession: B33098

R:Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: B33098
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <NIC>

Query Match 31.7%; Score 19; DB 2; Length 9;
Best Local Similarity 44.4%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GLDQRFSG 12
||| :||
Db 1 GLQTATXIG 9

RESULT 12

D57444

neuropeptide Grb-Asr B4 - two-spotted cricket

C:Species: *Gryllus bimaculatus* (two-spotted cricket)

C>Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996

C:Accession: D57444

R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.

J. Biol. Chem. 270, 21103-21108, 1995

A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the

A:Reference number: A57444; PMID:95403341; PMID:7673141

A:Accession: D57444

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <LOR>

Query Match 30.0%; Score 18; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 3.7e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ORFSG 12
||| :||
Db 3 ERFHG 7

RESULT 13

PT0251

Ig heavy chain CRD3 region (clone 2-109C) - human (fragment)

C:Species: *Homo sapiens* (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0251

R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; PMID:9108337; PMID:1899102

A:Accession: PT0251

A:Molecule type: DNA

A:Residues: 1-10 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 18; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.7e+03;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TORFS 11
||| :||
Db 1 SORPT 5

RESULT 14

PH0920

T-cell receptor beta chain V-D-J region (isolate 6) - rat (fragment)

C:Species: *Rattus norvegicus* (Norway rat)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C:Accession: PH0920

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle

A:Reference number: PH0891; PMID:92078857; PMID:1836012

A:Accession: PH0920
A:Molecule type: mRNA
A:Residues: 1-12 <GOL>
A:Experimental source: concanavalin A-activated lymphoblast
A>Note: the authors translated the codon CAG for residue 12 as Glu
C:Keywords: T-cell receptor

Query Match 30.0%; Score 18; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 4.4e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 AAEGIDT 7
:|:|:|
DB 4 SAQGANT 10

RESULT 15

PT0529
T-cell receptor beta chain V-D-J region (100-4K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0529
R:Reaney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:9127601; PMID:1711558
A:Accession: PT0529
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-7 <FEED>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 28.3%; Score 17; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAEGT 5
::|||
DB 2 SSEGL 6

Search completed: April 15, 2003, 10:21:19
Job time : 15 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 10:14:54 ; Search time 11 Seconds

(without alignments)
45.247 Million cell updates/sec

Title: US-09-521-527C-1

Perfect score: 60

Sequence: 1 AAEGLDTRFSG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 467

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	38.3	9	1	FAR6_CALVO
2	22	36.7	9	1	FAR5_CALVO
3	22	36.7	9	1	FAR7_CALVO
4	20	33.3	12	1	TKN2_KASMA
5	18	30.0	11	1	TKC2_CALVO
6	17	28.3	11	1	TKNA_RANRI
7	17	28.3	11	1	TKN_PHYFU
8	16	26.7	8	1	NPB_BOVIN
9	16	26.7	9	1	FIBB_MACFU
10	16	26.7	10	1	URAI_HUMAN
11	16	26.7	11	1	TKNA_CHICK
12	16	26.7	11	1	TKNA_GADMO
13	16	26.7	11	1	TKNA_HORSE
14	15	25.0	8	1	ALIS_CYDPO
15	15	25.0	8	1	FAR8_CALVO
16	15	25.0	9	1	FAR1_CALVO
17	15	25.0	9	1	FAR2_CALVO
18	15	25.0	9	1	FAR3_CALVO
19	15	25.0	9	1	FAR4_CALVO
20	15	25.0	9	1	FAR5_CALVO
21	15	25.0	9	1	FIBB_PAPNA
22	15	25.0	9	1	FIBB_PAPNA
23	15	25.0	9	1	FIBB_PAPNA
24	15	25.0	10	1	AMPN_HELAM
25	15	25.0	10	1	COXO_THIOB
26	15	25.0	10	1	TKN_PHYBI
27	15	25.0	11	1	FAR9_CALVO
28	15	25.0	11	1	TKN2_UPERU
29	15	25.0	11	1	TKNA_RANCA
30	15	25.0	12	1	SOI5_BACSU
31	15	25.0	12	1	UR2B_CATCO
32	14	23.3	8	1	CUP_THICU
33	14	23.3	10	1	PCK_FASHE

34	14	23.3	10	1	TKNB_CHICK	P19851	gallus gall
35	14	23.3	11	1	PVK1_PERAM	P41837	periplaneta
36	14	23.3	11	1	RR2_CONAM	P42341	conopholis
37	14	23.3	11	1	TKN1_UPEIN	P82026	uperoleia 1
38	14	23.3	11	1	TKN1_UPERU	P08612	uperoleia 1
39	13	22.5	10	1	FAR6_CALVO	P41867	calliphora
40	13	21.7	8	1	COXG_RAT	P80430	rattus norv
41	13	21.7	9	1	LM72_LOCOMI	P22396	locusta mig
42	13	21.7	9	1	CCAP_CARMA	P38556	carcinus ma
43	13	21.7	10	1	CA12_LITCI	P82086	litorea cit
44	13	21.7	10	1	CAER_LITXA	P56264	litorea xan
45	13	21.7	10	1	VEG6_BACSU	P80659	baclillus su

ALIGNMENTS

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RESULT 1
ID FAR6_CALVO STANDARD; PRT; 9 AA.
AC P41861;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Calliphmrfamide 6.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
OX NCBI_TaxId=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.,
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliphmrfamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992)
CC -!- SIMILARITY: BELONGS TO THE FAR6 (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC DR PIR: F41978; F41978.
CC KW Neuropeptide; Amidation.
CC FT MOD_RES 9
CC SQ SEQUENCE 9 AA: 1058 MW: 96010699CAB60865 CRC64:
Query Match 38.3%; Score 23; DB 1; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2 AAEGLDTRF 10
DB 1 ASGQDFMRF 9
RESULT 2
ID FAR5_CALVO STANDARD; PRT; 9 AA.
AC P41860;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Calliphmrfamide 5.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
OX NCBI_TaxId=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;

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RA	Dive H. Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA	Reifeld J.F., Thorpe A.;
RT	"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT	neuropeptides (designated callFMFamides) from the blowfly
RT	Calliphora vomitoria.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC	-1- SIMILARITY: BELONGS TO THE FAMR (FMRFAMIDE RELATED PEPTIDE)
CC	FAMILY.
DR	PIR: E41978; E41978.
KW	Neuropeptide; Amidation.
FT	MOD_RES
SO	SEQUENCE 9 AA; 1068 MW; 39D10699CAB6D867 CRC64;
Query Match	
Best Local Similarity 36.7%; Score 22; DB 1; Length 9;	
Matches 5; Conservative 0; Pred. No. 1.1e+05;	
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Oy	2 AEGDPTGRF 10
Db	1 AXGDDFMRF 9
RESULT 3	
FAR7_CALVO	
ID	FAR7_CALVO STANDARD; PRT; 9 AA.
AC	PA1862;
DT	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	01-NOV-1995 (Rel. 32, Last annotation update)
DE	CallFMRFamide 7.
OS	Calliphora vomitoria (Blue blowfly).
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC	Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
OX	NCBI_TaxID=27454;
LN	[1]
RP	SEQUENCE.
RC	TISSUE=Thoracic ganglion;
RX	MEDLINE=9216111; PubMed=1549595;
RA	Dive H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA	Reifeld J.F., Thorpe A.;
RT	"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT	neuropeptides (designated callFMFamides) from the blowfly
RT	Calliphora vomitoria.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC	-1- SIMILARITY: BELONGS TO THE FAMR (FMRFAMIDE RELATED PEPTIDE)
CC	FAMILY.
DR	PIR: G41978; G41978.
KW	Neuropeptide; Amidation.
FT	MOD_RES
SO	SEQUENCE 9 AA; 1081 MW; ELD10699CAB6D86A CRC64;
Query Match	
Best Local Similarity 36.7%; Score 22; DB 1; Length 9;	
Matches 5; Conservative 0; Pred. No. 1.1e+05;	
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Oy	2 AEGDPTGRF 10
Db	1 AXGDDFMRF 9
RESULT 4	
TKN2_KASMA	
ID	TKN2_KASMA STANDARD; PRT; 12 AA.
AC	P08614;
DT	01-AUG-1988 (Rel. 08, Created)
DT	01-AUG-1988 (Rel. 08, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	Hyambatin.
OS	Kassinia maculata (African rhacophorid frog) (Hylambates maculatus).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Hyperoliidae;
OC	Rhinoc.

Ox	NCB1_TaxID=8414;
RN	[1]
RP	SEQUENCE.
RA	Yasuhara T., Nakajima T., Ersperer G.F., Ersperer V.:
RT	"New tachykinins, Glut ₂ , Pro ⁶ -kassinin (hyalambates-kassinin) and hyalambatin, in the skin of the African rhacophorid frog Hyalambates maculatus.";
RL	Biomed. Res. 2:613-617(1981).
CC	-I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.
DR	P.I.: SIMILARITY; BELONGS TO THE TACHYKININ FAMILY. PIR: S07436; S07436. InterPro: IPR003580; Protachyklinn. DR InterPro: IPR002040; Tachyklnhn. Pfam: PF02202; Tachyklnhn; 1. SMART: SMART0203; TK; 1.
KW	PROSITE: PS00267; TACHYKININ; 1.
DQ	Tachykynlnhn; Neuropeptide; Amidation; Amphibian skin. MOD_RES 12 AMIDATION. FT SEQUENCE 12 AA; 1441 MW; 3287CD2EDD4A0AB7 CRC64;
Oy	Query Match Score 20; DB 1; Length 12; Best Local Similarity 57.1%; Pred. NO. 4.6e+02; Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
yq	6 DTORFSG 12 Db 4 DPDFRYG 10
RESULT 5	
ID	TKC2_CALVO STANDARD; PRT: 11 AA.
AC	P41518;
DT	01-NOV-1995 (Rel. 32, Created)
DF	01-NOV-1995 (Rel. 32, Last sequence update)
DE	Callitachykinn II.
OS	Calliphora vomitoria (Blue blowfly).
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliporidae; Calliphora.
OX	NCBI_TaxID=27454;
RN	[1]
RP	SEQUENCE, AND SYNTHESIS.
RX	MEDLINE=95075727; PubMed=7984492;
RA	Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J., Naessel D.R.;
RT	"Callitachykinn I and II, two novel myotropic peptides isolated from the blowfly, Calliphora vomitoria, that have resemblances to tachykinins.";
RL	Peptides 15:761-768(1994).
CC	-I- FUNCTION: MYOACTIVE PEPTIDE.
CX	-I- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW	Tachyknnhn; Neuropeptide; Amidation
FT	MOD_RES 11 AMIDATION. SQ SEQUENCE 11 AA; 1103 MW; 15DVE3FC9CDD44 CRC64;
Oy	Query Match Score 18; DB 1; Length 11; Best Local Similarity 44.4%; Pred. NO. 1.1e+03; Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
DB	4 GLDTORFSG 12 1 GIQNNAEVG 9
RESULT 6	
ID	TKNA_RANRI STANDARD; PRT: 11 AA. P29207;

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DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ranaklinin (Substance-P-related peptide).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
"Ranaklinin: a novel NK1 tachykinin receptor agonist isolated with
neurokinin B from the brain of the frog Rana ridibunda.";
RT J. Neurochem. 57:2086-2091(1991).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 28.3%; Score 17; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 QRFSG 12
Db 5 ERFYG 9

RESULT 7
TKN_PHYFU STANDARD; PRT; 11 AA.
AC P08615;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Physalaemin.
OS Physalaemus fuscumaculatus (Neotropical frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Leptodactylidae;
OC Physalaemus.
OX NCBI_TaxID=8378;
RN [1]
RP SEQUENCE.
RX MEDLINE=66076612; PubMed=5857249;
Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
"Structure and pharmacological actions of physalaemin, the main
active polypeptide of the skin of Physalaemus fuscumaculatus.";
RT Arch. Biochem. Biophys. 20:489-490(1964).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Amphibian skin.
FT MOD_RES 11 11 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.

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SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 28.3%; Score 17; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 DTQRFSG 12
Db 3 DPNKFYG 9

RESULT 8
NPB_BOVIN STANDARD; PRT; 8 AA.
ID NPB_BOVIN
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
Yang H.-Y.T., Pratta W., Majane E.A., Costa E.;
"Isolation, sequencing, synthesis, and pharmacological
characterization of two brain neuropeptides that modulate the action
of morphine.";
RT Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR: B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 TO NEUROPEPTIDE A (AA 5-8) (IDENTICAL).
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QRF 10
Db 6 QRF 8

RESULT 9
FIBB_MACFU STANDARD; PRT; 9 AA.
ID FIBB_MACFU
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
Nakamura S., Takenaka O., Takahashi K.;
"Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
patas monkey (Erythrocebus patas): their amino acid sequences,
restricted mutations, and a molecular phylogeny for macaques,
RT quensons, and baboons.";
RT J. Biochem. 97:1487-1492(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT

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CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.

CC -1 SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC -1 MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA 6 BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

DR PIR, C24180, C24180.

DR InterPro: IPR002181; Fibrinogen.C.

DR PROSITE: PS00514; FIBRIN_AG.C.DOMAIN: PARTIAL.

KW Blood coagulation; Plasma.

FT PEPTIDE 1 9 FIBRINOPEPTIDE B.

FT NON_TER 9 9

SO SEQUENCE 9 AA: 1038 MW: 69FE5B9C75BB1B CRC64:

Query Match 26.7%; Score 16; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 FSG 12

DB 6 FSG 8

RESULT 10

UNRAI_HUMAN STANDARD: PRT; 10 AA.

ID UNRAI_HUMAN

AC P32118:

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Unknown protein from 2D-page of red blood cells (Spot 1) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE.

RC TISSUE-Erythrocyte;

RX MEDLINE=9417970; PubMed=831871;

RA Colar O., Hughes G.J., Frutiger S., Paquet N., Bairoch A., Pasquail C., Sanchez J.C., Tissot J.-D., Appel R.D., Walzer C., Balant L., Hochstrasser D.F.,

RT "Plasma and red blood cell protein maps: update 1993."

RL Electrophoresis 14:1223-1231(1993).

CC -1 MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.4, ITS MW IS: 23 Kda.

DR SWISS-2DPAGE; P32118; HUMAN.

DR NON_TER 1 1

FT NON_TER 1 1

SO SEQUENCE 10 AA: 977 MW: 723C65B1AD0587B CRC64:

Query Match 26.7%; Score 16; DB 1; Length 10; Best Local Similarity 60.0%; Pred. No. 2.4e+03; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 EGLDT 7

DB 3 EGLDT 7

RESULT 11

TKNA_CHICK STANDARD: PRT; 11 AA.

ID TKNA_CHICK

AC P19850:

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Substance P.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Atherinomorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Gallus.

OX NCBI_Taxid=9031;

RN [1]

RP SEQUENCE.

RC TISSUE-Intestine; PubMed=2452461;

RX MEDLINE=88204263; PubMed=2452461;

RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;

RT "[Arg3]substance P and neuropeptide A from chicken small intestine."

RU Regul. Pept. 20:171-180(1988).

CC -1 FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.

CC -1 SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR: JN0023; JN0023.

DR InterPro: IPR003580; Protachykinin.

DR InterPro: IPR002040; Tachykinin.

DR Pfam: PF02202; Tachykinin; 1.

DR SMART: SM00203; TK; 1.

DR PROSITE: PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.

FT MOD_RES 11 11

SO SEQUENCE 11 AA: 1377 MW: 21487FE3C9D6CC7 CRC64:

Query Match 26.7%; Score 16; DB 1; Length 11; Best Local Similarity 60.0%; Pred. No. 2.7e+03; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 QRFSG 12

DB 5 QRFSG 9

RESULT 12

TKNA_GADMO STANDARD: PRT; 11 AA.

ID TKNA_GADMO

AC P28498;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Substance P.

OS Gadus morhua (Atlantic cod).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphia; Paracanthopterygii; Gadiformes; Gadidae; Gadus.

OX NCBI_Taxid=8049;

RN [1]

RP SEQUENCE.

RC TISSUE-Brain;

RX MEDLINE=92298992; PubMed=1376687;

RA Jensen J., Conlon J.M.;

RT "Substance-P-related and neuropeptide-A-related peptides from the brain of the cod and trout."

RU Eur. J. Biochem. 206:659-664(1992).

CC -1 FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.

CC -1 SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR InterPro: IPR003580; Protachykinin.

DR InterPro: IPR002040; Tachykinin.

DR Pfam: PF02202; Tachykinin; 1.

DR SMART: SM00203; TK; 1.

DR PROSITE: PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.

FT MOD_RES 11 11

SO SEQUENCE 11 AA: 1315 MW: 214860D759B6CC7 CRC64:

Query Match 26.7%; Score 16; DB 1; Length 11; Best Local Similarity 60.0%; Pred. No. 2.7e+03; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 QRFSG 12


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Db          5 QDFG 9

RESULT 13
TKNA_HORSE
ID          STANDARD:      PRT:      11 AA.
AC          P01290:
DT          21-JUL-1986 (Rel. 01, Created)
DT          21-JUL-1986 (Rel. 01, Last sequence update)
DT          30-MAY-2000 (Rel. 39, Last annotation update)
DE          Substance P.
GN          TAC1 OR NK1A OR TAC2 OR NKA.
OS          Equus caballus (horse), and
OC          Cavia porcellus (Guinea pig).
OC          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX          NCBI_TaxId=9796, 10141;
RN          [1]
RP          SEQUENCE.
RC          SPECIES-Horse;
RA          Studer R.O., Trzeciak A., Lergier W.;
RT          "Isolation and amino-acid sequence of substance P from horse
RT          intestine.";
RL          Helv. Chim. Acta 56:860-866(1973).
RN          [2]
RP          SEQUENCE.
RC          SPECIES=C.porcellus;
RX          MEDLINE=90044685; PubMed=2478925;
RA          Murphy R.;
RT          "Primary amino acid sequence of guinea-pig substance P.";
RL          Neuropeptides 14:105-110(1989).
CC          -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC          EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC          SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC          MUSCLES.
CC          -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR          PIR: A01558; SPHO.
DR          PIR: A0654; A0654.
DR          InterPro: IPR003580; Protachykinin.
DR          InterPro: IPR002040; Tachykinin.
DR          SMART: PF02202; Tachykinin; 1.
DR          SMART: SM00203; TK; 1.
DR          PROSITE: PS00267; TACHYKININ; 1.
KM          Tachykinin; Neuropeptide; Amidation; Neuropeptide.
FT          MOD_RES      11      11      AMIDATION.
SQ          SEQUENCE      11 AA; 1349 MW; 3E757EE3C9D6C6C7 CRC64;

Query Match
Best Local Similarity      26.7%; Score 16; DB 1; Length 11;
Matches      3; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

OY          8 QDFG 12
Db          5 QDFG 9

RESULT 14
ALIS_CYPDO
ID          STANDARD:      PRT:      8 AA.
AC          P82156:
DT          30-MAY-2000 (Rel. 39, Created)
DT          30-MAY-2000 (Rel. 39, Last sequence update)
DT          30-MAY-2000 (Rel. 39, Last annotation update)
DE          Cydlastatin 5.
OS          Cydia pomonella (Codling moth).
OC          Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC          Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC          Ditrysia; Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX          NCBI_TaxId=82600;
RN          [1]
RP          SEQUENCE.
RC          TISSUE=Larva;

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RX          MEDLINE=98054539; PubMed=9392829;
RA          Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA          Davey M., East P.D., Thorpe A.;
RT          "Lepidopteran peptides of the allatostatin superfamily.";
RL          Peptides 18:1301-1309(1997).
CC          -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM          Neuropeptide; Amidation.
FT          MOD_RES      8      8      AMIDATION.
SQ          SEQUENCE      8 AA; 898 MW; 922879CABB58640D CRC64;

Query Match
Best Local Similarity      25.0%; Score 15; DB 1; Length 8;
Matches      3; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

OY          2 AEGD 6
Db          1 ARGD 5

RESULT 15
FAR8_CALVO
ID          STANDARD:      PRT:      8 AA.
AC          P41863;
DT          01-NOV-1995 (Rel. 32, Created)
DT          01-NOV-1995 (Rel. 32, Last sequence update)
DT          01-NOV-1995 (Rel. 32, Last annotation update)
DE          CallifMRamide 8.
OS          Calliphora vomitoria (Blue blowfly).
OC          Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC          Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC          Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
OX          NCBI_TaxId=27454;
RN          [1]
RP          SEQUENCE.
RC          TISSUE=Thoracic ganglion;
RX          MEDLINE=92196111; PubMed=1549595;
RA          Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA          Rehfeld J.F., Thorpe A.;
RT          "Isolation, structure, and activity of -Phe-NH2-Arg-Phe-NH2
RT          neuropeptides (designated callifMRamides) from the blowfly
RT          Calliphora vomitoria.";
RL          Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC          -1- SIMILARITY: BELONGS TO THE FAR8 (PMRFAMIDE RELATED PEPTIDE)
CC          FAMILY.
DR          PIR: H41978; H41978.
KM          Neuropeptide; Amidation.
FT          MOD_RES      8      8      AMIDATION.
SQ          SEQUENCE      8 AA; 957 MW; 72D40699CAA44D8 CRC64;

Query Match
Best Local Similarity      25.0%; Score 15; DB 1; Length 8;
Matches      3; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

OY          6 DFOF 10
Db          4 DFOF 8

Search completed: April 15, 2003, 10:20:22
Job time : 12 secs

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 10:17:20 ; Search time 28 Seconds

(without alignments)
88.306 Million cell updates/sec

Title: US-09-521-527c-1

Perfect score: 60

Sequence: 1 AAEGDTRFSG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 2041

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioplasmid:*
17: sp_archaeplastid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	36.7	11	5	Q9TWM2
2	21	35.0	12	12	Q86570
3	19	31.7	8	5	Q94695
4	19	31.7	10	12	P90373
5	19	31.7	11	2	Q8RKN1
6	18	30.0	8	2	Q9R3X0
7	18	30.0	9	15	Q70140
8	18	30.0	10	11	Q9QVE6
9	18	30.0	11	9	Q9TOR6
10	17	28.3	8	4	Q9Y4J4
11	17	28.3	8	7	Q2S801
12	17	28.3	8	7	Q2S797
13	17	28.3	8	7	Q2S812
14	17	28.3	11	10	Q04131
15	17	28.3	12	4	Q9H3W2
16	17	28.3	12	6	Q9YR6

17	16	26.7	8	4	Q15895	Q15895	homo sapien
18	16	26.7	9	4	Q96P97	Q96P97	homo sapien
19	16	26.7	9	12	Q88612	Q88612	middelburg
20	16	26.7	10	2	Q8VN85	Q8VN85	helicobacte
21	16	26.7	11	5	Q23876	Q23876	dictyostell
22	16	26.7	11	6	P83128	P83128	bos indicus
23	16	26.7	11	6	Q9TRX0	Q9TRX0	sus scrofa
24	16	26.7	11	7	Q77899	Q77899	oreochromis
25	16	26.7	11	7	Q77900	Q77900	oreochromis
26	16	26.7	11	7	Q77901	Q77901	oreochromis
27	16	26.7	11	7	Q77902	Q77902	oreochromis
28	16	26.7	11	7	Q77903	Q77903	oreochromis
29	16	26.7	11	7	Q77904	Q77904	oreochromis
30	16	26.7	11	7	Q77905	Q77905	oreochromis
31	16	26.7	11	7	Q77916	Q77916	oreochromis
32	16	26.7	11	7	Q77917	Q77917	oreochromis
33	16	26.7	11	7	Q77921	Q77921	oreochromis
34	16	26.7	11	16	Q9K7A4	Q9K7A4	bacillus ha
35	16	26.7	12	2	Q93U04	Q93U04	escherichia
36	16	26.7	12	10	P82328	P82328	pisum sativ
37	16	26.7	12	11	Q925V7	Q925V7	mus musculu
38	15	25.0	8	5	Q94623	Q94623	manduca sex
39	15	25.0	9	2	Q43960	Q43960	azotobacter
40	15	25.0	9	2	P72149	P72149	pseudomonas
41	15	25.0	9	10	Q9AXH8	Q9AXH8	mesembryant
42	15	25.0	10	2	Q9LSW6	Q9LSW6	liberibacte
43	15	25.0	10	2	Q9S3J6	Q9S3J6	escherichia
44	15	25.0	10	2	Q9R5N1	Q9R5N1	clostridium
45	15	25.0	10	2	Q9R5N1	Q9R5N1	clostridium

ALIGNMENTS

RESULT 1
ID Q9TWM2 PRELIMINARY: PRT: 11 AA.
AC Q9TWM2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Buccalin B, BUCB.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidia;
OC Aplysiidae; Aplysia.
OX NCBI_Taxid=6500;
RN [1]
RP SEQUENCE.
RX MEDLINE=95083478; PubMed=7991459;
RA Villm F.S., Cropper E.C., Rosen S.C., Tenenbaum R., Kupfermann I.,
RA Weiss K.R.;
RT "Structure, localization, and action of buccalin B: a bioactive
RT peptide from Aplysia.";
RL Peptides 15:959-969(1994).
SQ SEQUENCE 11 AA; 1153 MW; 692253F9C9C86B44 CRC64;

Query Match 36.7%; Score 22; DB 5; Length 11;
Best local similarity 55.6%; Pred. No. 12e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 GUDTRFSG 12
DB 1 GLDTRFVG 9
RESULT 2
ID Q86570 PRELIMINARY: PRT: 12 AA.
AC Q86570;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
DE Small hepatitis delta antigen (Fragment).

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OS Hepatitis delta virus (HDV).
OC Viruses; Deltavirus.
OX NCBI_TaxID=12475;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93190623; PubMed=8447179;
RA Khudaykov Yu.E., Favovov M.O., Fields H.A.;
RT "A small open reading frame of the hepatitis delta virus antigenomic
RT RNA encodes a protein that elicits antibodies in some infected
RL Patients.";
RL Virus Res. 27:13-24(1993).
DR EMBL: S56617; AAB25696.1; -.
FT NON_TER
SQ SEQUENCE 12 AA; 1330 MW; 0E63E3FA15486400 CRC64;

Query Match
Best Local Similarity 35.0%; Score 21; DB 12; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EGLD 6
Db 1 EGLD 4

RESULT 3
Q94695 PRELIMINARY; PRT; 8 AA.
ID Q94695;
AC Q94695;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Actin (Fragment).
GN ARDC.
OS Physarum polycephalum (Slime mold).
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
OC Physarum.
OX NCBI_TaxID=5791;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96182101; PubMed=8622700;
RA Bernard M., Lagneel C., Pallotta D., Pierron G.;
RT "Mapping of a replication origin within the promoter region of two
RT unlinked, abundantly transcribed actin genes of Physarum
RT polycephalum.";
RL Mol. Cell. Biol. 16:968-976(1996).
DR EMBL: M73459; AAB03706.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; F4C6C2CAAB187B16 CRC64;

Query Match
Best Local Similarity 31.7%; Score 19; DB 5; Length 8;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGLDTQ 8
Db 2 EGEDVQ 7

RESULT 4
P90373 PRELIMINARY; PRT; 10 AA.
ID P90373;
AC P90373;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE U5 (Fragment).
OS Pseudorabies virus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10345;
RN [1]
RP SEQUENCE FROM N.A.
DR STRAIN=BECKER;

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RA Pederson N.E., Casey J.T., II, Koslowski K.M.;
RT "Pseudorabies virus UL6 and UL7 sequence.";
RL Submitted (Aug-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: U66829; AAB37266.1; -.
FT NON_TER
SQ SEQUENCE 10 AA; 859 MW; D232421DDDDDDDD CRC64;

Query Match
Best Local Similarity 31.7%; Score 19; DB 12; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAE6 4
Db 6 AAE6 9

RESULT 5
Q8RKN1 PRELIMINARY; PRT; 11 AA.
ID Q8RKN1;
AC Q8RKN1;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE beta-lactamase CTX-M-9 (Fragment).
GN BLACTX-M-9.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=743-D;
RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,
RA Prats G.;
RT "A novel complex sul1-type integron in Escherichia coli carrying the
RT bla(CTX-M-9) gene.";
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: A1092058; AAM15718.1; -.
FT NON_TER
SQ SEQUENCE 11 AA; 1071 MW; C26BF418D050440D CRC64;

Query Match
Best Local Similarity 31.7%; Score 19; DB 2; Length 11;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AEGL 5
Db 8 AEGL 11

RESULT 6
Q9R3X0 PRELIMINARY; PRT; 8 AA.
ID Q9R3X0;
AC Q9R3X0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
DE (Fragment).
GN RBCL.
OS Bacteria; Cyanobacteria; Oscillatoriales; Planctothrix.
OX NCBI_TaxID=59512;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BC-PLA 9316, AND BC-PLA 9303;
RX MEDLINE=20005589; PubMed=10537197;
RA Beard S.J., Handley B.A., Hayes P.K., Walsby A.E.;
RT "The diversity of gas vesicle genes in Planctothrix rubescens from
RT Lake Zurich.";
RL Microbiology 145:2757-2768(1999).
DR EMBL: A1132249; CAB59537.1; -.
DR EMBL: A1132248; CAB59534.1; -.

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FT  NON_TER 1 1
SQ  SEQUENCE 8 AA; 957 MW; 33DIAA685B19CB CRC64;

Query Match
Best Local Similarity 30.0%; Score 18; DB 2; Length 8;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EGLDT 7
   1 :|:|
   3 ESMdT 7

Db 3 ESMdT 7

RESULT 7
ID 070140 PRELIMINARY; PRT; 9 AA.
AC 070140:
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95194694; PubMed=7888189;
RA Gao F., Yue L., Craig S., Thornton C.L., Robertson D.L.,
RA McCutchan F.E., Bradac J.A., Sharp P.M., Hahn B.H.;
RT "Genetic variation of HIV type 1 in four World Health Organization-
RT sponsored vaccine evaluation sites: generation of functional envelope
RT (glycoprotein 160) clones representative of sequence subtypes A, B, C,
RT and E. WHO Network for HIV Isolation and Characterization.";
RL AIDS Res. Hum. Retroviruses 10:1359-1368(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=020;
RA MEDLINE=96190564; PubMed=8627686;
RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S.,
RA Karlsson G., Sedroski J., Morgado M., Galvao-Castro B.,
RA von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
RA Hahn B.H.;
RT "Molecular cloning and analysis of functional envelope genes from
RT human immunodeficiency virus type 1 sequence subtypes A through G. The
RT WHO and NIAID Networks for HIV Isolation and Characterization.";
RL J. Virol. 70:1651-1657(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=020;
RA Allen E.E.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U08794; AAB05175.1; -.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1098 MW; 5B76D40AB1AB01A3 CRC64;

Query Match
Best Local Similarity 30.0%; Score 18; DB 15; Length 9;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 DTORF 10
   1 :|:|
   4 ETRDF 8

Db 4 ETRDF 8

RESULT 8
ID 090VE6 PRELIMINARY; PRT; 10 AA.
AC 090VE6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Protamine MP2 Intermediate protein PMP2/26 (Fragment).

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OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinge A., Debarle M., Sautiere P., Chevallier P.;
RT "Molecular characterization of six intermediate proteins in the
RT processing of mouse protamine P2 precursor.";
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1028 MW; 2B099C75B72866D8 CRC64;

Query Match
Best Local Similarity 30.0%; Score 18; DB 11; Length 10;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGLDTPR 9
   1 :|:|
   4 QGLSPER 10

Db 4 QGLSPER 10

RESULT 9
ID 09TOR6 PRELIMINARY; PRT; 11 AA.
AC 09TOR6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAY-2002 (TReMBLrel. 20, Last annotation update)
DE Ner protein (Fragment).
OS Bacteriophage Mv.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC Mu-like viruses.
OX NCBI_TaxID=10677;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85153064; PubMed=6099259;
RA Krause H.M., Higgins N.P.;
RT "On the mu repressor and early DNA intermediates of transposition.";
RL Cold Spring Hard. Symp. Quant. Biol. 49:827-834(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92356834; PubMed=1386645;
RA Alazard R., Berthier M., Chandelier M.;
RT "Escherichia coli integration host factor stabilizes bacteriophage Mu
RT repressor interactions with operator DNA in vitro.";
RL Mol. Microbiol. 6:1707-1714(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92356835; PubMed=1386646;
RA Gama M.J., Tousseint A., Higgins N.P.;
RT "Stabilization of bacteriophage Mu repressor-operator complexes by the
RT Escherichia coli integration host factor protein.";
RL Mol. Microbiol. 6:1715-1722(1992).
DR EMBL: M10192; AAA32371.2; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1006 MW; 89978F816766987A CRC64;

Query Match
Best Local Similarity 30.0%; Score 18; DB 9; Length 11;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAEGL 5
   1 :|:|:
   2 AADGA 6

Db 2 AADGA 6

RESULT 10
ID 09Y4J4 PRELIMINARY; PRT; 8 AA.
AC 09Y4J4;

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DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE Runt/82nt/MTG8 protein (Fragment).
 GN Runt/82nt/MTG8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9502916; PubMed=7919324;
 RA Tjorne J.E., Calabi F.;
 RT "Alternative, out-of-frame runt/MTG8 transcripts are encoded by the
 RT derivative (8) chromosome in the t(8;21) of acute myeloid leukemia
 RT M2.";
 RL Blood 84:2115-2121(1994).
 DR EMBL: S74092; AAD1444.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 1067 MW; 20F414044B17244B CRC64;

Query Match 28.3%; Score 17; DB 7; Length 8;
 Best Local Similarity 42.9%; Pred. No. 6.7e+05;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 DTORFS 9
 DB 1 DTLDPS 7

RESULT 11
 ID Q29801 PRELIMINARY; PRT; 8 AA.
 AC Q29801;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HLA class II DR-beta chain (Fragment).
 GN HLA-DRB1*15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175156; PubMed=9110934;
 RA Svensson A.C., Setterblad N., Pihlgren U., Rask L., Andersson G.;
 RT "Evolutionary relationship between different human major
 RT histocompatibility complex HLA-DR haplotypes.";
 RL Immunogenetics 43:304-314(1996).
 DR EMBL: X88791; CAA61270.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 953 MW; C2C6C5B9CA731AA CRC64;

Query Match 28.3%; Score 17; DB 7; Length 8;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 DTORFS 11
 DB 1 DTLDPS 6

RESULT 12
 ID Q29797 PRELIMINARY; PRT; 8 AA.
 AC Q29797;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HLA class II DR-beta chain (Fragment).
 GN HLA-DRB1*01.

OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175156; PubMed=9110934;
 RA Svensson A.C., Setterblad N., Pihlgren U., Rask L., Andersson G.;
 RT "Evolutionary relationship between different human major
 RT histocompatibility complex HLA-DR haplotypes.";
 RL Immunogenetics 43:304-314(1996).
 DR EMBL: X88793; CAA61272.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 953 MW; C2C6C5B9CA731AA CRC64;

Query Match 28.3%; Score 17; DB 7; Length 8;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 DTORFS 11
 DB 1 DTLDPS 6

RESULT 13
 ID Q29812 PRELIMINARY; PRT; 8 AA.
 AC Q29812;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HLA class II DR-beta chain (Fragment).
 GN HLA-DRB6*01.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175156; PubMed=9110934;
 RA Svensson A.C., Setterblad N., Pihlgren U., Rask L., Andersson G.;
 RT "Evolutionary relationship between different human major
 RT histocompatibility complex HLA-DR haplotypes.";
 RL Immunogenetics 43:304-314(1996).
 DR EMBL: X88794; CAA61273.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 953 MW; C2C6C5B9CA731AA CRC64;

Query Match 28.3%; Score 17; DB 7; Length 8;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 DTORFS 11
 DB 1 DTLDPS 6

RESULT 14
 ID Q04131 PRELIMINARY; PRT; 11 AA.
 AC Q04131;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Wound induced protein (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OK NCBI_TaxID=4081;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=PIK-RED; TISSUE=PERICARP;
 RX MEDLINE=91355936; PubMed-1715787;
 RA Parsons B.L., Matroo A.K.;
 RT "Wound regulated accumulation of specific transcripts in tomato
 RT fruit: interactions with fruit development, ethylene and light.";
 RL Plant Mol. Biol. 17:453-464(1991).
 DR EMBL; X59884; CAA42539.1; -
 FT NON_TER
 SQ SEQUENCE 11 AA; 1278 MW; 92CB25782873325 CRC64;

Query Match 28.3%; Score 17; DB 10; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 EGLD 6
 :|||
 Db 6 KGLD 9

RESULT 15

O9H3W2 PRELIMINARY; PRT; 12 AA.
 AC O9H3W2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE TRE17 protein.
 GN TRE17 GENE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94010310; PubMed-8406013;
 RA Onno M., Nakamura T., Hillova J., Hill M.;
 RT "Identification of novel sequences in the repertoire of hypervariable
 RT TRE17 genes from immortalized nonmalignant and malignant human
 RT keratinocytes.";
 RT Gene 131:209-215(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93228825; PubMed-8471161;
 RA Onno M., Nakamura T., Mariage-Samson R., Hillova J., Hill M.;
 RT "Human TRE17 oncogene is generated from a family of homologous
 RT polymorphic sequences by single-base changes.";
 RL DNA Cell Biol. 12:107-118(1993).
 DR EMBL; X71371; CAC16150.1; -
 SQ SEQUENCE 12 AA; 1252 MW; 6E17AFDE83ADD87B CRC64;

Query Match 28.3%; Score 17; DB 4; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 EGLDT 7
 :|||
 Db 5 EGADS 9

Search completed: April 15, 2003, 10:20:58
 Job time : 30 secs

